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VERSION      AX137514.1  GI:14273708
KEYWORDS
SOURCE       common tobacco.
ORGANISM     Nicotiana tabacum.

REFERENCE
AUTHORS      Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
TITLE        Yamauchi, I., Nakashita, H., Yoshioka, K. and Doi, Y.
              Methods for transformation of plants, transformed plants and
              processes for preparation of polyesters
JOURNAL      Patent: EP 1076095-A 16 14-FEB-2001;
              Riken (JP)

FEATURES
  source     Location/Qualifiers
            127 bp  DNA
            28 a  24 c  45 g  30 t
BASE COUNT
ORIGIN
Query Match      47.1%; Score 85.8; DB 6; Length 127;
Best Local Similarity 97.8%; Pred. No. 7.8e-17;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5  TCCTCTCCCGCCGCTGTTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGG 64
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DB   11 TTGCTCTCCCGCCGCTGTTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGG 70
      |||

QY  65 GGCAGGATGGCTATATTCCTGGGAGGA 93
      |||
DB   71 GGCAGGATGGCTATATTCCTGGGAGCA 99
      |||

RESULT 5
LOCUS       E51179
DEFINITION  Process for producing polyester.
ACCESSION   E51179.1  GI:18629514
VERSION     JP 2001046074-A/16.
KEYWORDS    Nicotiana tabacum
SOURCE      Nicotiana tabacum
ORGANISM    Nicotiana tabacum

REFERENCE
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
JOURNAL      Nakashita, H., Yamauchi, I., Yoshioka, K. and Doi, Y.
              Processes for producing polyesters
              Patent: JP 2001046074-A 16 20-FEB-2001;
              RIKAGAKU KENKUSHO
COMMENT      OS Nicotiana tabacum (tobacco)
              PN JP 2001046074-A/16
              PD 20-FEB-2001
              PF 09-AUG-1999 JP 1999225839
              PR
              PI HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIOHARU DOI
              CC C12N15/00, A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC
              CC C12N15/00, C12N5/00

FEATURES
  source     Location/Qualifiers
            127 bp  DNA
            28 a  24 c  45 g  30 t
BASE COUNT
ORIGIN
Query Match      47.1%; Score 85.8; DB 6; Length 127;
Best Local Similarity 97.8%; Pred. No. 7.8e-17;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5  TCCTCTCCCGCCGCTGTTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGG 64
      |||
DB   11 TTGCTCTCCCGCCGCTGTTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGG 70
      |||

QY  65 GGCAGGATGGCTATATTCCTGGGAGGA 93
      |||
DB   71 GGCAGGATGGCTATATTCCTGGGAGCA 99
      |||

RESULT 6
LOCUS       TOCPNGVR
DEFINITION  Tobacco (N. tabacum) Val-tRNA gene and 16S rRNA gene 5' end.
ACCESSION   J01453
VERSION     J01453.1  GI:343519
KEYWORDS    16S ribosomal RNA; ribosomal RNA; transfer RNA; transfer RNA-Val.
              Tobacco (N. tabacum, var. bright yellow 4) chloroplast DNA, clone
              PTCL.
SOURCE      Chloroplast Nicotiana tabacum
ORGANISM    Chloroplast Nicotiana tabacum

REFERENCE
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
              Tondoh, N., Shinozaki, K. and Suglura, M.

```











COMMENT

On or before Jan 17, 2002 this sequence version replaced q1.264799.  
 q1.11807  
 The circular tobacco chloroplast DNA sequence is presented in a  
 linearized form by cutting at the junction (JLA) between IRA and  
 LSC. is designated zero and numbered proceeding towards LSC. The DNA  
 strand which codes for the large subunit of ribulose  
 1,5-bisphosphate carboxylase is designated as A strand and the  
 complementary strand as B strand.  
 Nucleotide sequence of IRA and L - 86686 (86686 bp) Inverted  
 repeat A (IRA) region (LSC): 112027 (25341 bp) Small single copy  
 region (SSC): 12028 - 130598 (18571 bp) Inverted repeat B  
 (IRB) region (LSC): 130599 - 130599 (2344 bp) An  
 inverted repeat C (IRC) region (LSC): 130599 - 130599 (2344 bp)  
 chloroplast 599793 NUCLEOTIDE NUMBER (FROM  
 SCOD)

112862  
 ara1 14569  
 ara2 14569  
 atpA 56777  
 atpB 55284  
 atpE 13452  
 atpH 14099  
 atpI 14099  
 atpJ 74507  
 infA 82495  
 matK 3658  
 ndhA 132231  
 ndhB 52667  
 ndhC 143365  
 ndhD 119025  
 ndhE 119955  
 ndhF 120709  
 ndhH 123116  
 ndhI 121609  
 ndhJ 51455  
 ndhK 51455  
 ORF70A 48941  
 ORF70B 102102  
 ORF70C 140524  
 ORF70D 131802  
 ORF70E 146070  
 ORF70F 96545  
 ORF70G 96119  
 ORF70H 66176  
 ORF70I 67588  
 ORF70J 96407  
 ORF70K 146219  
 ORF70L 102346  
 ORF70M 140280  
 ORF70N 111029  
 ORF70O 101769  
 ORF70P 139776  
 ORF70Q 130606  
 ORF70R 64335  
 ORF70S 77452  
 ORF70T 79043  
 ORF70U 58293  
 ORF70V 58293  
 ORF70W 43468  
 ORF70X 41208  
 ORF70Y 1595  
 ORF70Z 74953  
 ORF70A 35210  
 ORF70B 35210  
 ORF70C 71219  
 ORF70D 66868  
 ORF70E 77101  
 ORF70F 66485  
 ORF70G 7835  
 ORF70H 66726

30861  
 psbM 76680  
 psbN 76680  
 rbcL 57595  
 rbcL 154393  
 rpl14 88233  
 rpl14 88233  
 rpl14 85095  
 rpl20 71409  
 rpl22 86350  
 rpl22 154093  
 rpl23 88533  
 rpl23 10131  
 rpl23 10131  
 rpl36 82165  
 rpoA 81468  
 rpoB 27511  
 rpoC1 21342  
 rpoC2 21342  
 rpoE2 16937  
 rps3 85998  
 rps4 10107  
 rps4 10107  
 rps8 83006  
 rps8 142619  
 rps11 81950  
 rps11 141772  
 3 rps12 100854  
 5 rps12 36881  
 rps15 125491  
 rps16 6211  
 rps18 70518  
 rps18 70518  
 rps4.5 109240  
 rps4.5 133386  
 rns16 109599  
 rns16 133027  
 rns16 102761  
 rns23 138655  
 rns23 115293  
 trnA-UGC 105394  
 trnA-GCA 137232  
 trnD-GUC 28793  
 trnD-GUC 32007

Query Match 47.1a; Score 85.8; DB 8; Length 155939;  
 Best Local Similarity 97.8%; Pred. No. 1.6e-16; Indels 0; Gaps 0;  
 Matches 87; Conservative 0; Mismatches 2;  
 QY 5 TCGCTCCCGCCGCGTCTCAATGAGTGGATAGAGCGCTGGGGATTGACGTGAGG 64  
 DB 140064 TTGCTCCCGCCGCGTCTCAATGAGTGGATAGAGCGCTGGGGATTGACGTGAGG 140005  
 QY 65 GGCAGGAGTGCATATTTCTGSGAGCGCA 93  
 DB 140004 GGCAGGAGTGCATATTTCTGSGAGCGCA 139976

RESULT 12  
 LOCUS ABE316582 156687 bp DNA circular PLN 05-APR-2002  
 DEFINITION Atropa belladonna complete Plastid Chromosome, strain ADBP(AH).  
 ACCESSION AJ316582  
 KEYWORDS 16S ribosomal RNA; 23S ribosomal RNA; 4.5S ribosomal RNA; 5S  
 ribosomal RNA; accD gene; acetyl-CoA carboxylase beta subunit;  
 ATP-dependent protease; atpA gene; atpA subunit; atpA subunit;  
 beta subunit; atpA subunit; atpA subunit; atpA subunit; atpA  
 subunit; atpA subunit; atpA subunit; atpA subunit; atpA subunit;  
 atpH gene; atpI gene; catalytic subunit; ccsA gene; ccsA protein  
 required for heme-attachment to c-type cytochromes; ccmA  
 c1p gene; cyt b6/f complex subunit; cyt b6/f complex subunit;  
 b6/f complex subunit; b6/f complex subunit; b6/f complex subunit;  
 b6/f complex subunit; b6/f complex subunit; b6/f complex subunit;  
 deshydrogenase ND6 subunit; NADH dehydrogenase 18kD subunit; NADH  
 dehydrogenase 18kD subunit; NADH dehydrogenase 18kD subunit; NADH  
 dehydrogenase 18kD subunit; NADH dehydrogenase 18kD subunit; NADH  
 dehydrogenase ND4 subunit; NADH dehydrogenase ND4 subunit; NADH  
 dehydrogenase ND4 subunit; NADH dehydrogenase ND4L subunit; NADH



[illegible]

SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL REFERENCE AUTHORS	TITLE	JOURNAL	FEATURES SOURCE
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8	9	10	11	12	13	14
15	16	17	18	19	20	21
22	23	24	25	26	27	28
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386	387	388	389	390	391	392
393	394	395	396	397	398	399
400	401	402	403	404	405	406
407	408	409	410	411	41	

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Db 2 GCTCCCGCGCGCTGCTCAATGAGATGATAGAGAGGCTCTGGGATTGACGTGAGGGG 61  
QY 67 CAGGATGCGCTATATTTCTGGGAGGA 93  
|||||  
Db 62 CAGGGATGCGCTATATTTCTGGGAGGA 88  
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RESULT 15  
ARI17110  
LOCUS ARI17110 300 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 4 from patent US 6297054.  
ACCESSION ARI17110  
VERSION ARI17110.1 GI:17910560  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 300)  
AUTHORS Maliga,P., Carrier,H. and Chaudhuri,S.  
TITLE Editing-based selectable plasmid marker genes  
JOURNAL Patent: US 6297054  
FEATURES  
source 1..300 /organism="unknown"

BASE COUNT 90 a 63 c 86 g 61 t  
ORIGIN  
Query Match 46.9%; Score 85.4; DB 6; Length 300;  
Best Local Similarity 98.9%; Pred.No.1.le-16;  
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY - 7 GCTCCCGCGCGCTGCTCAATGAGATGATAGAGGCTCTGGGATTGACGTGAGGGG 66  
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Db 17 GCTCCCGCGCGCGCTGCTCAATGAGATGATAGAGGCTCTGGGATTGACGTGAGGGG 76  
|||||  
QY 67 CAGGATGCGCTATATTTCTGGGAGGA 93  
|||||  
Db 77 CAGGGATGCGCTATATTTCTGGGAGGA 103  
|||||

Search completed: May 25, 2003, 14:05:05  
Job time : 1177 secs



DB 6 GCTCCCGCCGCGCTGCTCAATGAGATGATAGAGCGCTCGTGGAATGACGTGAGGGG 65  
QY 67 CAGGATGCGTATATTTCTGGGAGGAGACACACACGCTTCCC 110  
DB 66 CAGGATGCGTATATTTCTGGGAGGAGACTCCGGGGGATTCAC 109

RESULT 3  
US-09-193-853-25  
; Sequence 25, Application US/09193853  
; Patent No. 6388168  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey V.  
; APPLICANT: Kuhlmoos, Lori A.  
; APPLICANT: Allison, Oles V.  
; APPLICANT: Carrer, Helaine  
; APPLICANT: Kanevski, Ivan  
; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; Expressing Recombinant Plasmids of Multicellular Plants and  
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Danna Dorfman, Herrell and Skillman  
; STREET: 601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19104-3907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/193.853  
; FILING DATE:  
; CLASSIFICATION: DATA:  
; PRIOR APPLICATION NUMBER: 08/189,256  
; FILING DATE:  
; PRIOR APPLICATION DATA: US 07/518,763  
; APPLICATION NUMBER:  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 129 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; RECOMBINATION: NO  
; ANTI-SENSE: NO  
; US-09-193-853-25 47.5% Score 86.4; DB 4; Length 129;  
Query Match  
Best Local Similarity 89.4%; Pred. No. 1.5e-20;  
Matches 93; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

DB 1 GCTCCCGCCGCGCTGCTCAATGAGATGATAGAGCGCTCGTGGAATGACGTGAGGGG 60  
QY 67 CAGGATGCGTATATTTCTGGGAGGAGACACACACGCTTCCC 110  
DB 66 CAGGATGCGTATATTTCTGGGAGGAGACTCCGGGGGATTCAC 109

RESULT 2  
US-08-189-256A-25  
; Sequence 25, Application US/08189256A  
; Patent No. 6388168  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora  
; APPLICANT: Staub, Jeffrey V.  
; APPLICANT: Kuhlmoos, Lori A.  
; APPLICANT: Allison, Oles V.  
; APPLICANT: Carrer, Helaine  
; APPLICANT: Kanevski, Ivan  
; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; Expressing Recombinant Plasmids of Multicellular Plants and  
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Danna Dorfman, Herrell and Skillman  
; STREET: 601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19104-3907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/189.256A  
; FILING DATE: 31-JAN-1994  
; CLASSIFICATION: DATA:  
; PRIOR APPLICATION NUMBER: 08/111,398  
; FILING DATE: 25-AUG-1993  
; PRIOR APPLICATION DATA: US 07/518,763  
; APPLICATION NUMBER:  
; FILING DATE: 01-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 129 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; RECOMBINATION: NO  
; ANTI-SENSE: NO  
; US-08-189-256A-25 47.5% Score 86.4; DB 2; Length 129;  
Query Match  
Best Local Similarity 89.4%; Pred. No. 1.5e-20;  
Matches 93; Conservative 0; Mismatches 11; Indels 0; Gaps 0;



RESULT 5  
US-09-193-853-19  
; Sequence 19, Application US/09193853



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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
COUNTRY: PA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE: 25-AUG-1993
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-18

Query Match 46.9%; Score 85.4; DB 2; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCGCTTCAATGAGATGATAGAGGCTGCTGGGATTGACGTGAGGGG 66
DB 23 GCTCCCGCCGCGCTTCAATGAGATGATAGAGGCTGCTGGGATTGACGTGAGGGG 66

QY 67 CAGGGATGCGCTATATTTCTGGGAGCGA 93
DB 83 CAGGGATGCGCTATATTTCTGGGAGCGA 109

RESULT 9
US-09-193-853-18
Sequence 18, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Kanevski, Ivan
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunn, Dorfman, Herrell and Skillman
STREET: 601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

STREET: 1601 Market Street Suite 720
CITY: Philadelphia
COUNTRY: PA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
CLASSIFICATION: 33
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE: 25-AUG-1993
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-18

Query Match 46.9%; Score 85.4; DB 2; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCGCTTCAATGAGATGATAGAGGCTGCTGGGATTGACGTGAGGGG 66
DB 23 GCTCCCGCCGCGCTTCAATGAGATGATAGAGGCTGCTGGGATTGACGTGAGGGG 66

QY 67 CAGGGATGCGCTATATTTCTGGGAGCGA 93
DB 83 CAGGGATGCGCTATATTTCTGGGAGCGA 109

RESULT 9
US-09-193-853-18
Sequence 18, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Kanevski, Ivan
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunn, Dorfman, Herrell and Skillman
STREET: 601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

STREET: 1601 Market Street Suite 720
CITY: Philadelphia
COUNTRY: PA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE: 25-AUG-1993
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-18

Query Match 46.9%; Score 85.4; DB 4; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCGCTTCAATGAGATGATAGAGGCTGCTGGGATTGACGTGAGGGG 66
DB 23 GCTCCCGCCGCGCTTCAATGAGATGATAGAGGCTGCTGGGATTGACGTGAGGGG 66

QY 67 CAGGGATGCGCTATATTTCTGGGAGCGA 93
DB 83 CAGGGATGCGCTATATTTCTGGGAGCGA 109

RESULT 10
US-08-189-256A-4
Sequence 4, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunn, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
```

1

FILING DATE: 07/25/75  
 PRIORITY APPLICATION DATA: US 07/518,763  
 APPLICATION NUMBER: 1-100  
 AFFILIATION: 1-100  
 AFFILIATION AGENT INFORMATION:  
 NAME: Reed, Janet E.  
 REGISTRATION NUMBER: 36,252  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 563-4044  
 TELEFAX: (215) 563-4044  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 55 base pairs  
 UNIT: base pairs  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHECAL: NO  
 RECOMBINANT: NO  
 UN-09-193-8534

Query Match	46.9%	Score 85.4;	DB 4;	Length 165;
Best Local Similarity	98.9%	Pred. No. 3.7e-20;		
			Indels	0: Gaps
			0: Mismatches	1:

Accession	Sequence	Position
1	GCTCCCCGGCGTCGTTCAATGAGAATGGAATGGAAGAGCGCTGCTGGGATTGACGTGAGGGGG	60
Db		
QY	67 CAGGGATGCGCTATATTTCTGGGAGGA	93
51	51 CAGGGATGCGCTATATTTCTGGGAGGA	87

RESULT 12  
US-08-189-256A-2  
Classification US/08189256A

APPLICANT: Svab, Zora  
 APPLICANT: Staub, Jeffrey  
 APPLICANT: Zoubenko, Oleg V.  
 APPLICANT: Allison, Helaine  
 APPLICANT: Kanevski, Ivan  
 TITLE OF INVENTION: DNA Constructs and Methods for Stably  
 Transforming Plastids of Higher Plants and  
 Title of Invention: Expressing Recombinant Proteins Therein  
 NUMBER OF PAGES: 47  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Dann, Dorfman, Herrell and Skillman  
 STREET: 1601 Market Street Suite 720  
 CITY: Philadelphia  
 STATE: PA  
 ZIP: 19103-2307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 SOFTWARE: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/189,256A  
 FILING DATE: 11-JAN-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/111,398  
 FILING DATE: 25-AUG-1993  
 PRIOR APPLICATION DATA: US 07/518,763  
 FILING DATE: 01-MAY-1990

## ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELEPHONE: (215) 563-4100

## TELEFAX: (215) 563-4044

## INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

LENGTH: 168 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-08-189-256A-2

Query Match 46.9%; Score 85.4; DB 2; Length 168;

Best Local Similarity 98.9%; Pred. No. 3.7e-20;

Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCTGGGATTCGACGTGAGGGG 66

Db 1 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCTGGGATTCGACGTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93

Db 61 CAGGGATGGCTATATTTCTGGGAGGCA 87

## RESULT 13

US-09-193-853-2

Sequence 2, Application US/09193853

Patent No. 6388168

## GENERAL INFORMATION:

APPLICANT: Malliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carriere, Helaine

APPLICANT: Kozlowski, Mark

TITLE OF INVENTION: DNA Constructs and Methods for Stably

Transforming Plastids of Multicellular Plants and

Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dunn, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT SEQUENCE DATA:

APPLICANT NUMBER: US/09/193,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,256

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/518,763

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4100

## TELEFAX: (215) 563-4044

## INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

LENGTH: 168 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-09-193-853-2

Query Match 46.9%; Score 85.4; DB 4; Length 168;

Best Local Similarity 98.9%; Pred. No. 3.7e-20;

Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCTGGGATTCGACGTGAGGGG 66

Db 1 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCTGGGATTCGACGTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93

Db 61 CAGGGATGGCTATATTTCTGGGAGGCA 87

## RESULT 14

US-09-283-419-3

Sequence 3, Application US/09283419A

Patent No. 6218145

## GENERAL INFORMATION:

APPLICANT: Bogosian, Gregg

APPLICANT: O'Neill, Julia P.

APPLICANT: Jeffrey, M.

TITLE OF INVENTION: Mitochondrial Expression Systems Based on Plastid or

Mitochondrial Promoter Combinations

FILE REFERENCE: MOPV040--

CURRENT APPLICATION NUMBER: US/09/283,419A

CURRENT FILING DATE: 1999-04-01

EARLIER APPLICATION NUMBER: 60/080,432

EARLIER FILING DATE: 1998-04-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 1-3

LENGTH: 184

TYPE: DNA

ORGANISM: Nicotiana tabacum.

US-09-283-419-3

Query Match 46.9%; Score 85.4; DB 4; Length 184;

Best Local Similarity 98.9%; Pred. No. 3.8e-20;

Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCTGGGATTCGACGTGAGGGG 66

Db 2 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCTGGGATTCGACGTGAGGGG 61

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93

Db 62 CAGGGATGGCTATATTTCTGGGAGGCA 88

## RESULT 15

US-08-189-256A-24

Sequence 24, Application US/08189256A

Patent No. 5877402

## GENERAL INFORMATION:

APPLICANT: Malliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carriere, Helaine

APPLICANT: Kozlowski, Mark

APPLICANT: Kanevski, Ivan

Search completed: May 25, 2003, 14:27:51  
Job time : 62 secs



us-09-762-105a-14.rnppb

Tue May 27 10:47:40 2003

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1  GACCTCCGCGCGCGCGCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTCAGCTG 60
   |||
1  GACCTCCGCTCCCGCGCGCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTCAGCTG 60
   |||

61  AGGGGGCAGGATGGCTATATTTCTGGGAG 90
   |||
61  AGGGGGCAGGATGGCTATATTTCTGGGAG 90
   |||

RESULT 4
US-09-940-925A-163
; Sequence 1, Application US/0940925A
; Publication No. US20030054338A1
; GENERAL INFORMATION:
; APPLICANT: MARY ANN D.
; APPLICANT: EMMICHIEY, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
;                 PARASITIC PROTOZOANS
; NUMBER OF SEQUENCES: 163
; FILE REFERENCE: PCT/US00/25930
; ADDRESS/SEE: MEDLEN & CARROLL
; CITY: SAN FRANCISCO
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MODIFIER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/940,925A
; FILING DATE: 10-Jun-2002
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL MEDLEN & CARROLL
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 397-8838
; INFORMATION FOR SEQ ID NO: 163:
; LENGTH: 144 base pairs
; TYPE: nucleic acid
; STRATEGY: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-09-940-925A-163
Query Match          46.6%; Score 84.8; DB 9; Length 144;
Best Local Similarity 97.7%; Pred. No. 2e-18; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 2;

QY 89 AGGAGACACACAGCTTTCCCATAGATAATTTGTTTACCTTAAGAGGAGATAT 148
   |||
DB 37 AGGAGACACACAGCTTTCCCTCTAGATAATTTGTTTACCTTAAGAGGAGATAT 96
   |||

QY 149 ACATATGCTGCTAGCATGCTGGTGACAG 176
   |||
DB 97 ACATATGCTGCTAGCATGCTGGTGACAG 124
   |||

RESULT 5
US-09-843-324A-1
; Sequence 1, Application US/09843324A
; Patent No. US20020042934A1
; GENERAL INFORMATION:
; APPLICANT: Staud, Jeffrey
; APPLICANT: Ye, Guangning
; APPLICANT:

US-10-109-812-1
; Sequence 1, Application US/10109812
; Publication No. US2003008081A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Paul
; APPLICANT: Cornille, Sylvie
; APPLICANT: Lutz, Kerry
; TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the
;                 Plant Cells of Higher Plants
; FILE REFERENCE: PCT/US00/0038 CIP
; PREFERENCE: Rutgers-00-0038 CIP
; CURRENT APPLICATION NUMBER: US/10/109,812
; PRIOR FILING DATE: 2002-03-29; US/00/25930
; PRIOR APPLICATION NUMBER: PCT/US00/25930
; PRIOR FILING DATE: 2000-06-13
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/211,139
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/155,007
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQUENCES: 163
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 130
; ORGANISM: tobacco
US-10-109-812-1
Query Match          49.5%; Score 90; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.1e-20; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;

QY 1  GACCTCCGCGCGCGCGCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTCAGCTG 60
   |||
DB 1  GACCTCCGCTCCCGCGCGCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTCAGCTG 60
   |||

QY 61  AGGGGGCAGGATGGCTATATTTCTGGGAG 90
   |||
DB 61  AGGGGGCAGGATGGCTATATTTCTGGGAG 90
   |||

RESULT 3
US-10-109-812-4
; Sequence 1, Application US/10109812
; Publication No. US2003008081A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Paul
; APPLICANT: Lutz, Kerry
; APPLICANT: Cornille, Sylvie
; TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the
;                 Plant Cells of Higher Plants
; FILE REFERENCE: PCT/US00/0038 CIP
; PREFERENCE: Rutgers-00-0038 CIP
; CURRENT APPLICATION NUMBER: US/10/109,812
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US00/25930
; PRIOR FILING DATE: 2000-06-13
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/211,139
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/155,007
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQUENCES: 163
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 131
; TYPE: DNA
; ORGANISM: tobacco
US-10-109-812-4
Query Match          49.5%; Score 90; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.1e-20; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
```



```

1 APPLICANT: Cornelle, Sylvie
2 APPLICANT: Letz, Kerry
3 TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the
4 TITLE OF INVENTION: Plasmids of Higher Plants
5 FILE REFERENCE: Rutgers-00-0038 CIP
6 CURRENT APPLICATION NUMBER: US/109,812
7 CURRENT FILING DATE: 2002-03-29
8 PRIOR APPLICATION NUMBER: PCT/US00/25930
9 PRIOR FILING DATE: 2000-09-21
10 PRIOR APPLICATION NUMBER: PCT/US00/211139
11 PRIOR FILING DATE: 2000-06-13
12 PRIOR APPLICATION NUMBER: 60/155,007
13 PRIOR FILING DATE: 1999-09-21
14 NUMBER OF SEQ ID NOS: 57
15 SOFTWARE: FastSeq for Windows-Version 3.0
16 SEQ ID NO 41
17 LENGTH: 89
18 TYPE: DNA
19 ORGANISM: Escherichia coli
20 US-10-085-612-41
21
22 Query Match 38.5%; Score 70; DB 9; Length 89;
23 Best Local Similarity 100.0%; Pred. No. 8,3e-14;
24 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
25
26 QY 88 GAGGAGGACCAACGGTTTCCCACTAGAAATAATTTGTTTAACATTTAAGAAGGAGATA 147
27 DB 19 GAGGAGGACCAACGGTTTCCCACTAGAAATAATTTGTTTAACATTTAAGAAGGAGATA 78
28
29 QY 148 TACATATGCC 157
30 DB 79 TACATATGCC 88
31
32 RESULT 8
33 US-10-085-476-12
34 Sequence 12, Application US/10085476
35 Patent No. US20020164722A1
36 GENERAL INFORMATION:
37 APPLICANT: J. Francisco, Raffaele
38 APPLICANT: Tommaso, Licia
39 APPLICANT: Behrens, Sven-Erik
40 TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
41 TITLE OF INVENTION: RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL
42 TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
43 FILE REFERENCE: IT0002PCA
44 CURRENT APPLICATION NUMBER: US/10/085,476
45 CURRENT FILING DATE: 2002-02-27
46 PRIOR APPLICATION NUMBER: 08/952,981
47 PRIOR FILING DATE: 1996-05-24
48 PRIOR APPLICANT: Behrens, Sven-Erik
49 PRIOR APPLICATION NUMBER: PCT/IT96/00106
50 PRIOR FILING DATE: 1996-05-24
51 PRIOR APPLICATION NUMBER: R495A000343
52 PRIOR FILING DATE: 1995-05-25
53 NUMBER OF SEQ ID NOS: 14
54 SOFTWARE: FastSeq for Windows Version 4.0
55 SEQ ID NO 12
56 LENGTH: 399
57 TYPE: RNA
58 ORGANISM: Rattus norvegicus
59 US-10-085-476-12
60
61 Query Match 38.0%; Score 69.2; DB 9; Length 399;
62 Best Local Similarity 68.9%; Pred. No. 3,1e-13;
63 Matches 51; Conservative 20; Mismatches 3; Indels 0; Gaps 0;
64
65 QY 90 GGGAGGACCAACGGTTTCCCACTAGAAATAATTTGTTTAACATTTAAGAAGGAGATA 149
66 DB 1 GGGAGGACCAACGGTTTCCCACTAGAAATAATTTGTTTAACATTTAAGAAGGAGATA 60
67
68 QY 150 CATATGCCAACCAT 163
69 DB 61 CAUATGCGCAUAT 74

```

Tue May 27 10:47:40 2003

DB 3364 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 3423

QY 149 ACATATGCCAACA 162  
DB 3424 ACATATGCCAACA 3437

RESULT 11  
US-09-987-107-51  
Sequence 51, Application US/09987107  
Patent No. US20020156007A1  
APPLICANT: GRAVERSEN, Jonas  
APPLICANT: GRAVERSEN, Joren  
TITLE OF INVENTION: APOLOPOPROTEINS ANALOGUES  
CURRENT APPLICATION NUMBER: US/09/987,107  
CURRENT FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/264,022  
PRIOR FILING DATE: 2001-01-15  
PRIOR APPLICATION NUMBER: DK PA2001 00057  
PRIOR FILING DATE: 2001-01-15  
PRIOR APPLICATION NUMBER: DK PA2000 01682  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 51  
LENGTH: 1057  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PT7 H6 Fx Cys-Apo A1 plasmid  
LOCATION: CDS  
OTHER INFORMATION:  
US-09-987-107-51

Query Match 36.7% Score 66.8; DB 9; Length 1057;  
Best Local Similarity 97.1% Fred. No. 3e-12; 2; Indels 0; Gaps 0;  
Matches 68; Conservative 0; Mismatches 0;

QY 89 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 148  
DB 36 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 95

QY 149 ACATATGCCA 158  
DB 96 ACATATGCCA 105

RESULT 12  
US-09-987-107-49  
Sequence 49, Application US/09987107  
Patent No. US20020156007A1  
APPLICANT: GRAVERSEN, Jones  
APPLICANT: GRAVERSEN, Joren  
TITLE OF INVENTION: APOLOPOPROTEINS ANALOGUES  
CURRENT APPLICATION NUMBER: US/09/987,107  
CURRENT FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/264,022  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: DK PA2001 00057  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: DK PA2000 01682  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 49  
LENGTH: 1088  
TYPE: DNA  
ORGANISM: Artificial Sequence

RESULT 9

US-09-897-776A-17  
Sequence 17, Application US/09897776A  
Publication No. US20030092001A1  
APPLICANT: Schnable, Patrick S.  
APPLICANT: Liu, Feng  
APPLICANT: Fan, Yan  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING MULTIPLE  
START CODONS AND HISTIDINE TAGS  
CURRENT APPLICATION NUMBER: US/09/897,776A  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 05/732,990  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 06/0169,725  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 160  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated oligonucleotide  
US-09-897-776A-17

Query Match 37.8% Score 68.8; DB 9; Length 97;  
Best Local Similarity 94.6% Fred. No. 2e-13; 0; Indels 0; Gaps 0;  
Matches 70; Conservative 0; Mismatches 2;

QY 89 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 148  
DB 17 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 76

QY 149 ACATATGCCAAG 160  
DB 77 ACATATGCCAAG 88

RESULT 10  
US-09-813-718-9  
Sequence 9, Application US/09813718  
Publication No. US20020182666A1  
APPLICANT: Wakasugi, Paul  
APPLICANT: Wakasugi, Kelsuke  
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For  
The Regulation of Angiogenesis  
CURRENT APPLICATION NUMBER: US/09/813,718  
CURRENT FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 5018  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3429)..(4879)  
OTHER INFORMATION: full-length tPrs in pET20B  
US-09-813-718-9

Query Match 37.1% Score 67.6; DB 9; Length 5018;  
Best Local Similarity 94.6% Fred. No. 3.3e-12;  
Matches 70; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 89 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 148  
DB 89 AGGGAGACCAACGGTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATAT 148

FEATURE:  
NAME/KEY: CDS  
OTHER INFORMATION:  
US-09-987-107-49

Query Match 36.7% Score 66.8; DB 9; Length 1088;  
Best Local Similarity 97.1%; Pred. No. 3.1e-12;  
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148  
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95  
QY 149 ACATATGGCA 158  
DB 96 ACATATGGGA 105

RESULT 13  
US-09-987-107-47  
Sequence 47, Application US/09987107  
Patent No. US20020156007A1  
GENERAL INFORMATION:  
APPLICANT: GRAVERSEN, Jonas  
APPLICANT: MOESTRUP, Soren  
FILE REFERENCE: APOLIPOPROTEINS ANALOGUES  
CURRENT APPLICATION NUMBER: US/09/987,107  
CURRENT FILING DATE: 2001-11-13  
PRIOR FILING DATE: 2001-01-26/264,022  
PRIOR APPLICATION NUMBER: DK PA2001 00057  
PRIOR FILING DATE: 2001-01-15  
PRIOR APPLICATION NUMBER: DK PA2000 01682  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 53  
LENGTH: 1217  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pT7 H6 Trip-A-Apo A-1 - Ampr plasmid  
NAME/KEY: CDS  
LOCATION: (100)...(1047)  
OTHER INFORMATION:

Query Match 36.7% Score 66.8; DB 9; Length 1217;  
Best Local Similarity 97.1%; Pred. No. 3.2e-12;  
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148  
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95  
QY 149 ACATATGGCA 158  
DB 96 ACATATGGGA 105

RESULT 14  
US-09-987-107-53  
Sequence 53, Application US/09987107  
Patent No. US20020156007A1  
GENERAL INFORMATION:  
APPLICANT: GRAVERSEN, Jonas  
APPLICANT: MOESTRUP, Soren  
FILE REFERENCE: APOLIPOPROTEINS ANALOGUES  
CURRENT APPLICATION NUMBER: US/09/987,107

CURRENT FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/264,022  
PRIOR FILING DATE: 2001-01-26  
FILE REFERENCE: APOLIPOPROTEINS ANALOGUES  
CURRENT APPLICATION NUMBER: US/09/987,107  
CURRENT FILING DATE: 2001-11-13  
PRIOR FILING DATE: 2001-01-26/264,022  
PRIOR APPLICATION NUMBER: DK PA2001 00057  
PRIOR FILING DATE: 2001-01-15  
PRIOR APPLICATION NUMBER: DK PA2000 01682  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 53  
LENGTH: 1217  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pT7H6 Trip-A-Apo A1 K9A K15A - Ampr plasmid  
NAME/KEY: CDS  
LOCATION: (100)...(1047)  
OTHER INFORMATION:  
US-09-987-107-53

Query Match 36.7% Score 66.8; DB 9; Length 1217;  
Best Local Similarity 97.1%; Pred. No. 3.2e-12;  
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148  
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95  
QY 149 ACATATGGCA 158  
DB 96 ACATATGGGA 105

RESULT 15  
US-09-987-107-55  
Sequence 55, Application US/09987107  
Patent No. US20020156007A1  
GENERAL INFORMATION:

APPLICANT: GRAVERSEN, Jonas  
APPLICANT: MOESTRUP, Soren  
FILE REFERENCE: APOLIPOPROTEINS ANALOGUES  
CURRENT APPLICATION NUMBER: US/09/987,107  
CURRENT FILING DATE: 2001-11-13  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: US 60/264,022  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: DK PA2001 00057  
PRIOR FILING DATE: 2001-01-15  
PRIOR APPLICATION NUMBER: DK PA2000 01682  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 55  
LENGTH: 1238  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 - Ampr plasmid  
NAME/KEY: CDS  
LOCATION: (100)...(1068)  
OTHER INFORMATION:  
US-09-987-107-55

Query Match 36.7% Score 66.8; DB 9; Length 1238;  
Best Local Similarity 97.1%; Pred. No. 3.2e-12;  
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148  
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95  
QY 149 ACATATGGCA 158  
DB 96 ACATATGGGA 105

Tue May 27 10:47:40 2003

DB 96 ACATATGGGA 105

Search completed: May 25, 2003, 14:29:51  
Job time : 107 secs

us-09-762-105a-14.rnpb

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 13:23:39 ; Search time 1416 Seconds  
(without alignments)  
2081.623 Million cell updates/sec

Title: US-09-762-105a-14  
Erfact score: 182  
Sequencer: 1 gactctgctccccccgctc.....tgacttggtgacagctagc 182

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

##### EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estinv:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_est3:\*
- 12: gb\_est4:\*
- 13: gb\_est5:\*
- 14: gb\_estfun:\*
- 15: em\_estom:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pil:\*
- 21: em\_gss\_pil:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_man:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	72.6	39.9	797 17	BH558942
2	72.2	39.7	735 17	BH548823 BOHRL72TR
3	72.2	39.7	735 17	BH558942
4	72.2	39.7	838 17	BH472349 BOCIY45TF
5	71.8	39.5	770 17	BH668002 BOHNL95TF
6	71.8	39.5	836 17	BH709230 BOHNC33TR

7	71.8	39.5	841 17	BH653765
8	71.6	39.3	724 17	BH418480
9	71.1	39.0	805 17	BH474481 BOHRY09TR
10	70.8	38.9	797 17	BH558942
11	70.8	38.9	735 17	BH548823 BOHRL72TR
12	70.8	38.9	199 17	BH579552
13	70.8	38.9	238 17	BH677595
14	70.8	38.9	292 17	BH677595
15	70.8	38.9	305 17	BH474703 BOGQ149TF
16	70.8	38.9	322 17	BH646726 BOCHN48TF
17	70.8	38.9	367 17	BH705426 BOHAG13TR
18	70.8	38.9	367 17	BH430502 BOHJD65TR
19	70.8	38.9	368 17	BH493122 BOHRC38TF
20	70.8	38.9	368 17	BH493122 BOHRC38TF
21	70.8	38.9	419 17	BH668002 BOHNL95TF
22	70.8	38.9	419 17	BH668002 BOHNL95TF
23	70.8	38.9	422 17	BH475597 BOG154TF
24	70.8	38.9	423 17	BH653681 BOHNSV92TR
25	70.8	38.9	434 17	BH545732 BOGK099TR
26	70.8	38.9	434 17	BH545732 BOGK099TR
27	70.8	38.9	441 17	BH678091 BOHGLJ20TR
28	70.8	38.9	441 17	BH678091 BOHGLJ20TR
29	70.8	38.9	448 17	BH657205 BOHMF25TR
30	70.8	38.9	450 17	BH657205 BOHMF25TR
31	70.8	38.9	451 17	BH725279 BOHMY87TR
32	70.8	38.9	451 17	BH725279 BOHMY87TR
33	70.8	38.9	456 17	BH541747 BOGPN81TF
34	70.8	38.9	468 17	BH740372 QK3410.1b
35	70.8	38.9	469 17	BH718684 BOHMLA51TR
36	70.8	38.9	475 17	BH659610 BOHPL27TR
37	70.8	38.9	475 17	BH659610 BOHPL27TR
38	70.8	38.9	482 17	BH700638 BOHMC243TF
39	70.8	38.9	482 17	BH700638 BOHMC243TF
40	70.8	38.9	484 17	BH649351 BOHKE288TF
41	70.8	38.9	484 17	BH649351 BOHKE288TF
42	70.8	38.9	487 17	BH650341 BOHML06TF
43	70.8	38.9	487 17	BH650341 BOHML06TF
44	70.8	38.9	489 17	BH649375 BOHLL37TR
45	70.8	38.9	489 17	BH649375 BOHLL37TR
46	70.8	38.9	501 17	BH717042 BOHYN88TR
47	70.8	38.9	501 17	BH717042 BOHYN88TR
48	70.8	38.9	503 17	BH654995 BOHMC341TR
49	70.8	38.9	506 17	BH641130 BOHMC23TF
50	70.8	38.9	507 17	BH491584 BOGTC15TR
51	70.8	38.9	508 17	BH675079 BOHML501TF
52	70.8	38.9	508 17	BH675079 BOHML501TF
53	70.8	38.9	511 17	BH717427 BOHKEP19TF
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#### ALIGNMENTS

RESULT 1  
BH558942  
LOCUS  
DEFINITION  
BOHRL72TR BOHL Brassica oleracea genomic clone BOHRL72, DNA  
sequence.  
ACCESSION  
BH558942  
VERSION  
BH558942.1  
KEYWORDS  
GSS  
SOURCE  
Brassica oleracea  
ORGANISM  
Brassica oleracea  
REFERENCE  
1 (bases 1 to 787)  
Tom, C.B., Van Aken, S., Utterback, T. and Fraser, C.M.  
Whole genome sequencing of Brassica oleracea  
Rosidae; eusoids II; Brassicales; Brassicaceae; Brassica.  
COMMENT  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: ctown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq Primer: read ends  
Class: Shotgun  
Location/Qualifiers  
source 1..787

FEATURES	source	Location/Qualifiers	base count	ORIGIN	Query Match	Match	Score	Length	0;
		1..775			39.8%	72.4;	DB 17;	Length 775;	
		/organism="Bacillus oleracea"			Similarity 87.8%;	Pred. No. 2.5e-12;			
		/db_xref="taxon:3712"			Conservative 11;	Mismatches 11;	Indels 0;	Gaps	
		/clone="BOHN79"							
		/clone_11b="BOH-PhoSI. Site.1: BstXI; 2-3 kb sheared							
		genomic DNA inserted into phoSI using BstXI linkers"							
		161 c	247 g	164 t					
BASE COUNT	203 a								
ORIGIN									
Qy	4	CTCGTCCCGCCGCGCTCTGATGAGATGATAGAGCGCTCGTGCGGATTTGACGTGAGG	63						
Qy	4	CTCGTCCCGCCGCGCTCTGATGAGATGATAGAGCGCTCGTGCGGATTTGACGTGAGG	63						
Db	8	CTTTCCTCCCTGCTGTTCGAAATAGAGATGAGCGCTCGTGCGGATTTGACGTGAGG	67						
Qy	64	GGCGAGGAGTGGCTATATTTCTGGGAGCA	93						
Qy	65	CTTTCCTCCCTGCTGTTCGAAATAGAGATGAGCGCTCGTGCGGATTTGACGTGAGG	97						
Db	65	CTTTCCTCCCTGCTGTTCGAAATAGAGATGAGCGCTCGTGCGGATTTGACGTGAGG	97						

TIGR  
 7712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtonnet@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.

Location/Qualifiers  
 1..838

/organism="Brassica oleracea"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone\_lib="BO.2.3\_KB"  
 /note="Vector: pBstXI; Site\_1: BstXI; 2-3 kb sheared genomic DNA inserted into pBstXI using BstXI linkers"

BASE COUNT 233 a 142 c 191 g 272 t  
 ORIGIN

Query Match 39.7% Score 72.2; DB 17; Length 838;  
 Best Local Similarity 86.0%; Pred. No. 2.9e-12;  
 Matches 0; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 CTCGCTCCCGCCGCTCAATGAGATGAAGAGCGCTGGGATTGACGTGAG 63  
 Db 720 CTTCGCTCCCGCTCAATGAGATGAAGAGCGCTGGGATTGACGTGAG 779  
 QY 64 GGGCAGGAGGCTATATTTCTGGGAGGAGAC 96  
 Db 780 GGGTAGGGGTAGCTATATTTCTGGGAGGAGAC 812

RESULT 5  
 BH68002  
 LOCUS  
 DEFINITION  
 VERSION  
 ACCESSION  
 SOURCE  
 ORGANISM

BH68002  
 BOMLN95TF BO.2.3\_KB Brassica oleracea genomic clone BOMLN95, DNA  
 sequence.  
 BH68002.1 GI:18727985  
 TIGR  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 770)  
 Town.C.D., Van Aken.S., Utterback.T. and Fraser.C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 unpublished (2001)  
 Contact: Chris Town

TIGR  
 7712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtonnet@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.

Location/Qualifiers  
 1..770

/organism="Brassica oleracea"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone\_lib="BO.2.3\_KB"  
 /note="Vector: pBstXI; Site\_1: BstXI; 2-3 kb sheared genomic DNA inserted into pBstXI using BstXI linkers"

BASE COUNT 204 a 162 c 246 g 158 t  
 ORIGIN

Query Match 39.5% Score 71.8; DB 17; Length 770;  
 Best Local Similarity 86.8%; Pred. No. 3.8e-12;

Matches 79; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 3 CTCGCTCCCGCCGCTCAATGAGATGAAGAGCGCTGGGATTGACGTGAG 62  
 Db 1 CTTCGCTCCCGCTCAATGAGATGAAGAGCGCTGGGATTGACGTGAG 60  
 QY 63 GGGCAGGAGGCTATATTTCTGGGAGGGA 93  
 Db 61 GGGTAGGGGTAGCTATATTTCTGGGAGGGA 91

RESULT 6  
 BH709230  
 LOCUS

DEFINITION  
 VERSION  
 ACCESSION  
 SOURCE  
 ORGANISM

BH709230  
 BOMN033TF BO.2.3\_KB Brassica oleracea genomic clone BOMN033, DNA  
 sequence.  
 BH709230.1 GI:18796385  
 TIGR  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Town.C.D., Van Aken.S., Utterback.T. and Fraser.C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 unpublished (2001)  
 Other.GSSs: BOMN033TF  
 Contact: Chris Town  
 TIGR  
 7712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtonnet@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.

Location/Qualifiers  
 1..836

/organism="Brassica oleracea"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone\_lib="BO.2.3\_KB"  
 /note="Vector: pBstXI; Site\_1: BstXI; 2-3 kb sheared genomic DNA inserted into pBstXI using BstXI linkers"

BASE COUNT 233 a 146 c 195 g 262 t  
 ORIGIN

Query Match 39.5% Score 71.8; DB 17; Length 836;  
 Best Local Similarity 86.0%; Pred. No. 3.9e-12;  
 Matches 100; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 4 CTCGCTCCCGCCGCTCAATGAGATGAAGAGCGCTGGGATTGACGTGAG 63  
 Db 664 CTTCGCTCCCGCTCAATGAGATGAAGAGCGCTGGGATTGACGTGAG 723  
 QY 64 GGGCAGGAGGCTATATTTCTGGGAGGAGACACACGGTTTCCCACTAGAAATAT 123  
 Db 724 GGGTAGGGGTAGCTATATTTCTGGGAGGAGACACCTCATCGCATATGAGCGCGGTGATAC 783  
 QY 124 TTGTTTAACTTTAAGACGAGGATATAC 150  
 Db 784 AAGTATGACTTGGAAATGAAGAAATTC 810

RESULT 7  
 BH653765  
 LOCUS

DEFINITION  
 VERSION  
 ACCESSION  
 SOURCE  
 ORGANISM

BH653765  
 BOMN133TF BO.2.3\_KB Brassica oleracea genomic clone BOMN133, DNA  
 sequence.  
 BH653765.1 GI:18796385  
 TIGR  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

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VERSION      BH653765.1  GI:18711917
KEYWORDS     Brassica oleracea.
SOURCE       GSS.
ORGANISM     Brassica oleracea.

REFERENCE    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS      T. (bases 1 to 724), W. Aken, S., Utterback, T. and Fraser, C.M.
TITLE        Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Contact: Chris Town
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Email: cdownt@ti.gr.org
              Seq primer: TR doubled haploid provided by Tom Osborn.
              Class: sheared ends.
              Location/Qualifiers
                1..724
                /strain="Brassica oleracea"
                /db_xref="taxon:3712"
                /clone="BOGK95"
                /vector="pUC19"
                /note="vector: pUC19; Site_1: BstXI; 2-3 kb sheared
              genomic DNA inserted into pUC19 using BstXI linkers"
              genomic DNA 151 a 229 g 150 g 194 t

BASE COUNT   221 a 139 c 182 g 263 t
ORIGIN
Query Match      39.0%; Score 71.6; DB 17; Length 724;
Best Local Similarity 85.1%; Pred. No. 4.4e-12;
Matches 80; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 4 CTCGCCCCCGCGCTGTCATGAGATGATGATGAGAGGCTCTGGGATTGACGTGAGG 63
Db 675 CTTCGCTCCCTCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 734
OY 64 GGGCAGGATGCGTATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 123
Db 735 GGGTAGGCTAGCTATATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 794
OY 124 TTTTATGCTTGAAGGAGGATATAC 150
Db 795 AAGTATGACTTGGAAATGAACATTC 821

RESULT 8
LOCUS      BH418480/c
DEFINITION BOGK95TR BOX Brassica oleracea genomic clone BOGK95, DNA
ACCESSION  BH418480.1  GI:17604208
VERSION     BH418480.1  GI:17604208
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
ORGANISM    Brassica oleracea.

REFERENCE    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS      T. (bases 1 to 724), W. Aken, S., Utterback, T. and Fraser, C.M.
TITLE        Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Contact: Chris Town
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Email: cdownt@ti.gr.org
              Seq primer: TR doubled haploid provided by Tom Osborn.
              Class: sheared ends.
              Location/Qualifiers
                1..724
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                /db_xref="taxon:3712"
                /clone="BOGK95"
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                /note="vector: pUC19; Site_1: BstXI; 2-3 kb sheared
              genomic DNA inserted into pUC19 using BstXI linkers"
              genomic DNA 221 a 139 c 182 g 263 t

BASE COUNT   221 a 139 c 182 g 263 t
ORIGIN
Query Match      39.0%; Score 71.6; DB 17; Length 805;
Best Local Similarity 84.2%; Pred. No. 7e-12;
Matches 80; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4 CTGCGTCCCGCGCTGTCATGAGATGATGATGATGATGATGATGATGATGATGATG 63
Db 707 CTTCGCTCCCTCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 648
OY 64 GGGCAGGATGCGTATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 97
Db 647 GGGTAGGCTAGCTATATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 614

RESULT 9
LOCUS      BH474481
DEFINITION BOH9Y09TR BOH9 Brassica oleracea genomic clone BOH9Y09, DNA
ACCESSION     BH474481.1  GI:17682592
VERSION        BH474481.1  GI:17682592
KEYWORDS        GSS.
SOURCE          Brassica oleracea.
ORGANISM        Brassica oleracea.

REFERENCE    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS      T. (bases 1 to 805), S., Utterback, T. and Fraser, C.M.
TITLE        Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Other_GSSs: BOH9Y09TF
              Contact: Chris Town
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Fax: 301-838-0208
              Email: cdownt@ti.gr.org
              Seq primer: TR doubled haploid provided by Tom Osborn.
              Class: sheared ends.
              Location/Qualifiers
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                /db_xref="taxon:3712"
                /clone="BOH9Y09"
                /vector="pUC19"
                /note="vector: pUC19; Site_1: BstXI; 2-3 kb sheared
              genomic DNA inserted into pUC19 using BstXI linkers"
              genomic DNA 221 a 139 c 182 g 263 t

BASE COUNT   221 a 139 c 182 g 263 t
ORIGIN
Query Match      39.0%; Score 71.6; DB 17; Length 805;
Best Local Similarity 84.2%; Pred. No. 7e-12;
Matches 80; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4 CTGCGTCCCGCGCTGTCATGAGATGATGATGATGATGATGATGATGATGATGATG 63
Db 707 CTTCGCTCCCTCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 648
OY 64 GGGCAGGATGCGTATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 97
Db 647 GGGTAGGCTAGCTATATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 614

RESULT 9
LOCUS      BH474481
DEFINITION BOH9Y09TR BOH9 Brassica oleracea genomic clone BOH9Y09, DNA
ACCESSION     BH474481.1  GI:17682592
VERSION        BH474481.1  GI:17682592
KEYWORDS        GSS.
SOURCE          Brassica oleracea.
ORGANISM        Brassica oleracea.

REFERENCE    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS      T. (bases 1 to 805), S., Utterback, T. and Fraser, C.M.
TITLE        Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Other_GSSs: BOH9Y09TF
              Contact: Chris Town
              9712 Medical Center Drive, Rockville, MD 20850, USA.
              Tel: 301-838-3523
              Fax: 301-838-0208
              Email: cdownt@ti.gr.org
              Seq primer: TR doubled haploid provided by Tom Osborn.
              Class: sheared ends.
              Location/Qualifiers
                1..805
                /strain="Brassica oleracea"
                /db_xref="taxon:3712"
                /clone="BOH9Y09"
                /vector="pUC19"
                /note="vector: pUC19; Site_1: BstXI; 2-3 kb sheared
              genomic DNA inserted into pUC19 using BstXI linkers"
              genomic DNA 221 a 139 c 182 g 263 t

BASE COUNT   221 a 139 c 182 g 263 t
ORIGIN
Query Match      39.0%; Score 71.6; DB 17; Length 805;
Best Local Similarity 84.2%; Pred. No. 7e-12;
Matches 80; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4 CTGCGTCCCGCGCTGTCATGAGATGATGATGATGATGATGATGATGATGATGATG 63
Db 707 CTTCGCTCCCTCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 648
OY 64 GGGCAGGATGCGTATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 97
Db 647 GGGTAGGCTAGCTATATTTCTGGAGGAGGACCAACGCTTTCCCACTAGAAATATT 614

```



Db 697 CTTGCTCCCTCCGCTGTCGATGAATGAAGGCTCTGGGATTGACGTGAGG 756  
 QY 64 GGGCAGGAGTGCTATATTTCTGGAGGACCA 98  
 Db 757 GGGTAGGGTACGATATTTCTGGAGGCACTCA 791

RESULT 10  
 BH721450  
 LOCUS BH721450 847 bp DNA linear GSS 20-FEB-2002  
 DEFINITION BOMFR11TR\_BO\_2.3\_KB Brassica oleracea genomic clone BOMFR11, DNA  
 sequence.  
 ACCESSION BOMFR11  
 VERSION BH721450.1 GI:16823465  
 KEYWORDS GSS  
 SOURCE Brassica oleracea.  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 847)  
 Authors: Tom Osborn, S. Utterback, T. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 unpublished (2001)  
 Other GSSs: BOMFR11TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 For additional information, see <http://www.tigr.org/tdb/at/at.html>  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..847  
 /organism="Brassica oleracea"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="lib=BO\_2.3\_KB"  
 /note="Vector: pBOS1; site: 1; BstXI: 2-3 kb sheared genomic DNA inserted into pBOS1 using BstXI linkers"

BASE COUNT 239 a 145 c 200 g 263 t

Query Match 39.0%; Score 71; DB 17; Length 847;  
 Best Local Similarity 84.2%; Pred. No. 7; le-12;  
 Matches 80; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 4 CTTGCTCCCTCCGCTGTCGATGAATGAAGGCTCTGGGATTGACGTGAGG 63  
 Db 641 CTTGCTCCCTCCGCTGTCGATGAATGAAGGCTCTGGGATTGACGTGAGG 700

QY 64 GGGCAGGAGTGCTATATTTCTGGAGGAGCA 98  
 Db 701 GGGTAGGGTACGATATTTCTGGAGGCACTCA 735

RESULT 11  
 AQ962940/c  
 LOCUS LERG142TR LERG Arabidopsis thaliana genomic clone LERG142, DNA  
 sequence.  
 ACCESSION AQ962940  
 VERSION AQ962940.1 GI:6790641  
 KEYWORDS GSS  
 SOURCE thale cress  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 169)

AUTHORS Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterback, T.,  
 Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.  
 TITLE Genomic survey sequencing of Landsberg erecta ecotype of  
 Arabidopsis thaliana and identification of sequence-based  
 polymorphisms (2000)  
 JOURNAL Molecular Biology and Evolution  
 COMMENT Contact: Xiaoying Lin  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: at@tigr.org  
 For additional information, see <http://www.tigr.org/tdb/at/at.html>  
 Seq primer: TR  
 Class: shotgun.

FEATURES  
 source  
 1..169  
 /organism="Arabidopsis thaliana"  
 /strain="Landsberg erecta"  
 /db\_xref="taxon:3702"  
 /clone="LERG142"  
 /note="Organism: Leaf; Vector: pUC19TK; Total genomic DNA was  
 sheared to 0.4-0.7 kbp before ligation."

BASE COUNT 46 a 49 c 27 g 47 t

Query Match 38.9%; Score 70.8; DB 17; Length 169;  
 Best Local Similarity 86.7%; Pred. No. 9e-12;  
 Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4 CTTGCTCCCTCCGCTGTCGATGAATGAAGGCTCTGGGATTGACGTGAGG 63  
 Db 161 CTTGCTCCCTCCGCTGTCGATGAATGAAGGCTCTGGGATTGACGTGAGG 102

QY 64 GGGCAGGAGTGCTATATTTCTGGAGGCA 93  
 Db 101 GGGTAGGGTACGATATTTCTGGAGGCA 72

RESULT 12  
 BH537952  
 LOCUS BOGFU38TR BOGF Brassica oleracea genomic clone BOGFU38, DNA  
 sequence.  
 ACCESSION BH537952  
 VERSION BH537952.1 GI:17776124  
 KEYWORDS GSS  
 ORGANISM Brassica oleracea.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 199)  
 Authors: Tom, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 unpublished (2001)  
 Other GSSs: BOGFU38TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 For additional information, see <http://www.tigr.org/tdb/at/at.html>  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 1..199  
 /organism="Brassica oleracea"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"

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/clone="BOGW48"
/clone_lib="BOGP"
/notes="vector: phos1; site_1: BatXI; 2-3 kb sheared
genomic DNA inserted into phos1 using BatXI linkers"
BASE COUNT      53 a 34 c 55 g 57 t
ORIGIN
Query Match      38.9%; Score 70.8; DB 17; Length 199;
Best Local Similarity 86.7%; Pred. No. 5.3e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4 CTCGCTCCCGCCGCTGTCATGAGATGATAGAGCGCTCGGCGATTGACGTGAGG 63
Db 58 CTCGCTCCCGCCGCTGTCATGAGATGATAGAGCGCTCGGCGATTGACGTGAGG 117
QY 64 GGGCAGGATGCTGATATTTCTGGGAGGA 93
Db 118 GCGTAGGGTAGCTATATTTCTGGGAGGA 147

RESULT 13
BH677595
LOCUS      BOMCM49TR BO_2_3_KB Brassica oleracea genomic clone BOMCM49, DNA
DEFINITION BOMCM49TR BO_2_3_KB Brassica oleracea genomic clone BOMCM49, DNA
ACCESSION BH677595
VERSION    BH677595
KEYWORDS   Brassica oleracea.
SOURCE     Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 238) S., Utterback,T. and Fraser,C.M.
           Whole genome shotgun sequencing of Brassica oleracea
           Unpublished (2001)
AUTHORS    Contact: Chris Town
TITLE      9712 Medical Center Drive, Rockville, MD 20850, USA.
JOURNAL    Tel: 301-838-3523
COMMENT    Fax: 301-838-0208
           Email: cdtown@nigr.org
           DNA is from a doubled haploid provided by Tom Osborn.
           Seq primer: 5'
           Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..238
     organism="Brassica oleracea"
     eukaryote="Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
     spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
     rosidae; eurosids II; Brassicales; Brassicaceae; Brassica."
     clone="BOMCM49"
     db_xref="taxon:3712"
     /clone_lib="BOGP"
     /notes="vector: phos1; site_1: BatXI; 2-3 kb sheared
     genomic DNA inserted into phos1 using BatXI linkers"
BASE COUNT      63 a 41 c 67 g 67 t
ORIGIN
Query Match      38.9%; Score 70.8; DB 17; Length 238;
Best Local Similarity 86.7%; Pred. No. 5.6e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4 CTCGCTCCCGCCGCTGTCATGAGATGATAGAGCGCTCGGCGATTGACGTGAGG 63
Db 99 CTCGCTCCCGCCGCTGTCATGAGATGATAGAGCGCTCGGCGATTGACGTGAGG 158
QY 64 GGGCAGGATGCTGATATTTCTGGGAGGA 93
Db 159 GCGTAGGGTAGCTATATTTCTGGGAGGA 188

RESULT 14
BH74703

```

```

LOCUS      BH74703
DEFINITION BOMQ449TF BOQG Brassica oleracea genomic clone BOMQ49, DNA
sequence.
ACCESSION BH74703
VERSION    BH74703
KEYWORDS   Brassica oleracea.
SOURCE     Brassica oleracea.
ORGANISM   Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 292)
AUTHORS    Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE      Whole genome shotgun sequencing of Brassica oleracea
JOURNAL    Other GSSs: BOMQ49TR
COMMENT    Contact: Chris Town
           TIGR Medical Center Drive, Rockville, MD 20850, USA.
           Tel: 301-838-3523
           Fax: 301-838-0208
           Email: cdtown@nigr.org
           DNA is from a doubled haploid provided by Tom Osborn.
           Seq primer: 5'
           Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..292
     organism="Brassica oleracea"
     eukaryote="Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
     spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
     rosidae; eurosids II; Brassicales; Brassicaceae; Brassica."
     clone="BOMQ49"
     /clone_lib="BOGP"
     /notes="vector: phos1; site_1: BatXI; 2-3 kb sheared
     genomic DNA inserted into phos1 using BatXI linkers"
BASE COUNT      83 a 79 g 80 t
ORIGIN
Query Match      30.9%; Score 70.8; DB 17; Length 292;
Best Local Similarity 86.7%; Pred. No. 5.9e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4 CTCGCTCCCGCCGCTGTCATGAGATGATAGAGCGCTCGGCGATTGACGTGAGG 63
Db 92 CTCGCTCCCGCCGCTGTCATGAGATGATAGAGCGCTCGGCGATTGACGTGAGG 151
QY 64 GGGCAGGATGCTGATATTTCTGGGAGGA 93
Db 152 GCGTAGGGTAGCTATATTTCTGGGAGGA 181

RESULT 15
BH646726/c
BOMWR48TF.1 BO_2_3_KB Brassica oleracea genomic clone BOMWR48, DNA
sequence.
ACCESSION BH646726
VERSION    BH646726
KEYWORDS   Brassica oleracea.
SOURCE     Brassica oleracea.
ORGANISM   Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 305)
AUTHORS    Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE      Whole genome shotgun sequencing of Brassica oleracea
JOURNAL    Other GSSs: BOMWR48TF
COMMENT    Contact: Chris Town
           TIGR Medical Center Drive, Rockville, MD 20850, USA.
           Tel: 301-838-3523
           Fax: 301-838-0208

```

Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: 5' ends.  
Class: Shred  
Location/Qualifiers  
1..305  
/organism="Brassica oleracea"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOGR48"  
/clone\_lib="BO\_2\_3\_KB"  
/notes="Vector: PHOS1; Site\_1: BstXI; 2-3 kb sheared  
genomic DNA inserted into PHOS1 using BstXI linkers."  
88 a 85 c 57 g 75 c

BASE COUNT  
ORIGIN

Query Match 38.9%; Score 70.8; DB 17; Length 305;  
Best Local Similarity 86.7%; Pred. No. 6e-12;  
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 4 CTGCTCCCGCGCTCGTTCATGAGATGATGATGAGGCTCTCGGATTGACCTGAGG 63  
DB 102 CTTCCTCCCTCGCTGATGATGATGATGATGAGGCTCTCGGATTGACCTGAGG 43  
OY 64 GGGCAGGAGTGCTATATTCTGGGAGGGA 93  
DB 42 GGGTAGGGTAGCTATATTCTGGGAGGCA 13

Search completed: May 25, 2003, 14:26:40  
Job time : 1420 secs



GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 12:31:19 : Search time 210 Seconds

(without alignments)  
1951.732 Million cell updates/sec

Title: US-09-762-105A-14

Record score: 182  
Sequence: 1 gactgtctcccgcgtc.....tgactgtggacagctacg 182

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DA seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SID82/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID82/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
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5: /SID82/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
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22: /SID82/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID82/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID82/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	182	100.0	182	21	AAZ61373	Nucleotide sequenc
2	182	100.0	1961	21	AAZ61384	Nucleotide sequenc
3	182	100.0	5263	21	AAZ61386	Nucleotide sequenc
4	159.4	87.3	161	21	AAZ61374	Nucleotide sequenc
5	111.2	61.1	168	21	AAZ61875	Nucleotide sequenc
6	111.2	61.1	168	22	AAZ61875	prn/G10L promoter
7	111.2	61.1	168	22	AAZ62552	Nucleotide sequenc
8	111.2	61.1	168	22	AAZ57902	Prn/G10L promoter
9	93.6	51.4	191	21	AAZ61361	Nucleotide sequenc

10	93.6	51.4	227	21	AAZ61360	Nucleotide sequenc
11	93.6	51.4	227	21	AAZ61362	Nucleotide sequenc
12	93.6	51.4	1049	22	AAZ61268	DNA fragment desig
13	93.6	51.4	195	21	AAZ61382	Nucleotide sequenc
14	92.2	50.7	185	21	AAZ61372	Nucleotide sequenc
15	92.2	50.7	185	21	AAZ61372	Nucleotide sequenc
16	92.2	50.7	195	21	AAZ61368	Nucleotide sequenc
17	90	49.5	130	22	AAZ61256	Plastid rRNA opero
18	90	49.5	131	22	AAZ61256	Plastid rRNA opero
19	90	49.5	154	21	AAZ61364	Nucleotide sequenc
20	90	49.5	159	21	AAZ61366	Nucleotide sequenc
21	90	49.5	195	21	AAZ61365	Nucleotide sequenc
22	90	49.5	195	21	AAZ61367	Nucleotide sequenc
23	90	49.5	195	21	AAZ61367	Nucleotide sequenc
24	90	49.5	185	21	AAZ61383	Nucleotide sequenc
25	89.6	49.2	171	16	AAZ61453	Prn/G10L promoter
26	89	48.9	183	21	AAZ61371	Nucleotide sequenc
27	89	48.9	201	21	AAZ61370	Nucleotide sequenc
28	86.4	47.5	129	20	AAZ61430	Regulatory region
29	86	47.3	140	20	AAZ61424	Regulatory region
30	86	47.3	164	20	AAZ61431	Regulatory region
31	85.8	47.1	127	22	AAZ64276	DNA of upstream re
32	85.8	47.1	107	22	AAZ65291	Phage gene 10, ss
33	85.8	47.1	6477	22	AAZ65291	Phage gene 10, ss
34	85.4	46.9	161	20	AAZ61423	Prn promoter sequ
35	85.4	46.9	165	20	AAZ61409	Prn/rbcl/Rubisco
36	85.4	46.9	168	20	AAZ61407	Tobacco plastid RR
37	85.4	46.9	184	22	AAZ69143	Regulatory region
38	85.4	46.9	258	20	AAZ61429	Plastid targeting
39	85.4	46.9	1134	18	AAZ61595	Selectable marker
40	85.4	46.9	1134	20	AAZ61415	Regulatory region
41	85.4	46.9	1134	21	AAZ61376	Regulatory region
42	85.4	46.9	1134	20	AAZ61415	Regulatory region
43	85.4	46.9	1416	20	AAZ61432	Plastid targeting
44	85.4	46.9	1417	18	AAZ61596	Plastid targeting
45	85.4	46.9	2962	20	AAZ61408	targetting region

## ALIGNMENTS

RESULT 1	
ID	AAZ61373 standard; DNA; 182 BP.
XX	AAZ61373;
AC	AAZ61373;
XX	19-JUN-2000 (first entry)
DT	
DE	Nucleotide sequence of chimeric promoter Prnrr17g10+DB/Ec.
DE	Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
XX	Prn promoter; protein expression; vaccine; enzyme; 17 phage gene 10, ss.
KW	Synthetic.
OS	
XX	
FT	Key
FT	Location/Qualifiers
FT	promoter
FT	7..89
FT	/*tag- a
FT	/*note- "Prn plastid promoter"
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FT	/*note- "Shine-Dalgarno sequence"
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XX	WO200007431-A1.
PN	
XX	17-FEB-2000.
PD	
XX	03-AUG-1999;
XX	99WO-US17806.
XX	
PR	03-AUG-1998;
PR	98US-0095163.
PR	03-AUG-1998;
PR	98US-0095167.
PR	15-DEC-1998;
PR	98US-0112257.

```
PR 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Malliga P, Kuroda H, Khan MS;
XX
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plasmids of higher plants, includes promoter, a
XX leader sequence and a downstream box element
XX
XX Claim 4; Fig 3D; 164pp; English.
XX
XX The present sequence represents a chimeric plastid RNA operon
XX omega-type (prn) promoter with the T7 phage gene 10, expressing
XX downstream box element, to produce recombinant DNA constructs for expressing
XX heterologous proteins in the plasmids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used for pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes. Plants which can be transformed with the constructs
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX
XX Sequence 182 BP; 49 A; 34 C; 56 G; 43 T; 0 other;
XX
XX Query Match 100.0%; Score 182; DB 21; Length 182;
XX Best Local Similarity 100.0%; Positives 128; Indels 0; Gaps 0;
XX Matches 182; Conservative 0; Mismatches 0;
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XX 1 GAGCTGCTCCCGCCGCGCTTCATGAGATGATGAGAGCTCGGTGGATGACGCTG 60
XX |||||||
XX 1 GAGCTGCTCCCGCCGCGCTTCATGAGATGATGAGAGCTCGGTGGATGACGCTG 60
XX |||||||
XX 61 AGGGGGCAGGATGCGTATATTTCTGGAGGAGACACACGCTTCCCTAGAAATA 120
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XX 61 AGGGGGCAGGATGCGTATATTTCTGGAGGAGACACACGCTTCCCTAGAAATA 120
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XX 121 ATTTTGTAACTTTAAGAGAGATATACATATGCGACGATGCTGGTGGACGCTA 180
XX |||||||
XX 121 ATTTTGTAACTTTAAGAGAGATATACATATGCGACGATGCTGGTGGACGCTA 180
XX |||||||
XX 181 GC 182
XX
XX 181 GC 182
XX
XX RESULT 2
XX AA261384
XX ID AA261384 standard; DNA; 1961 BP.
XX
XX AA261384;
XX
XX 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of DNA construct FLARE11-S3.
XX
XX Green fluorescent protein; GFP; ada; protein expression; vaccine;
XX
XX haemoglobin; enzyme; psba; T7 phage gene 10; ss.
XX
XX Synthetic
XX
XX Unidentified.
XX
XX Aqueorea victoria.
XX
XX
XX Key Location/Qualifiers
XX misc_feature 7-176
XX /note= "T7 phage gene 10 downstream box"
XX 218..1001
XX /note= "ada sequence"
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XX /note= "green fluorescent protein region"
XX 1035..1755
XX /tag= d
XX /note= "psba region"
XX
XX WO200007431-A1.
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Malliga P, Kuroda H, Khan MS;
XX
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plasmids of higher plants, includes promoter, a
XX leader sequence and a downstream box element
XX
XX Disclosure: Fig 32; 164pp; English.
XX
XX The present sequence represents a DNA construct of the invention.
XX The invention describes recombinant DNA constructs for expressing
XX heterologous proteins in the plasmids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used for pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes. Plants which can be transformed with the constructs
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX
XX Sequence 1961 BP; 552 A; 430 C; 486 G; 493 T; 0 other;
XX
XX Query Match 100.0%; Score 182; DB 21; Length 1961;
XX Best Local Similarity 100.0%; Positives 196; Indels 0; Gaps 0;
XX Matches 197; Conservative 0; Mismatches 0;
XX
XX 1 GAGCTGCTCCCGCCGCGCTTCATGAGATGATGAGAGCTCGGTGGATGACGCTG 60
XX |||||||
XX 1 GAGCTGCTCCCGCCGCGCTTCATGAGATGATGAGAGCTCGGTGGATGACGCTG 60
XX |||||||
XX 61 AGGGGGCAGGATGCGTATATTTCTGGAGGAGACACACGCTTCCCTAGAAATA 120
XX |||||||
XX 61 AGGGGGCAGGATGCGTATATTTCTGGAGGAGACACACGCTTCCCTAGAAATA 120
XX |||||||
XX 121 ATTTTGTAACTTTAAGAGAGATATACATATGCGACGATGCTGGTGGACGCTA 180
XX |||||||
XX 121 ATTTTGTAACTTTAAGAGAGATATACATATGCGACGATGCTGGTGGACGCTA 180
XX |||||||
XX 181 GC 182
```

```

Db      181 GC 182

RESULT 3
AAZ61386/C
ID      AAZ61386 standard; DNA; 5263 BP.
XX
XX
XX
AC      AAZ61386;
XX
XX      19-JUN-2000 (first entry)
XX
XX      Nucleotide sequence of plasmid pMSK49.
XX
XX      aadA; protein expression; vaccine; haemoglobin; enzyme; psbA;
KW      T7 phage gene 10; downstream box; green fluorescent protein; ss.
XX
XX      Synthetic.
XX
XX      Key
FH      misc_feature
FT      1..1860
FT      /tag= a
FT      /note= "Rice left targeting sequence"
FT      misc_feature
FT      1904..2092
FT      /tag= b
FT      /note= "psbA sequence"
FT      misc_feature
FT      2103..2823
FT      /tag= c
FT      /note= "green fluorescent protein sequence"
FT      misc_feature
FT      3682..3851
FT      /tag= d
FT      /note= "T7 phage gene 10 downstream box"
FT      misc_feature
FT      3877..5263
FT      /tag= e
FT      /note= "Rice right targeting sequence"
XX
XX      WO200007431-A1.
XX
XX      17-FEB-2000.
XX
XX      03-AUG-1999; 99WO-US17806.
XX
XX      03-AUG-1998; 98US-0095163.
XX
XX      03-AUG-1998; 98US-0095167.
XX
XX      15-DEC-1998; 98US-0112257.
XX
XX      29-APR-1999; 98US-0131611.
XX
XX      11-JUN-1999; 98US-0138764.
XX
XX      (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX      Maliga P, Kuroda H, Khan MS;
PI
XX      WPI; 2000-205525/18.
XX
XX      New recombinant DNA constructs, for expressing high levels of
XX      heterologous protein in plastids of higher plants, includes promoter, a
XX      leader sequence and a downstream box element -
XX
XX      Disclosure: Fig 3A-B, 164pp; English.
XX
XX      The present sequence represents a vector of the invention. The
XX      specification describes recombinant DNA constructs for expressing
XX      heterologous proteins in the plastids of higher plants. The DNA
XX      constructs comprise a 5' regulatory region which includes a promoter
XX      element, a leader sequence and a downstream box element operably linked
XX      to a coding region of the heterologous protein. The chimeric regulatory
XX      region enhances translational efficiency of an mRNA molecule encoded by
XX      the DNA construct. The DNA constructs are used for producing transformed
XX      monocot and dicot plants having high levels of heterologous protein
XX      in plastids. The DNA constructs are also used for producing transgenic
XX      crops and for pharmaceutical production of proteins including
XX      enzymes, antibodies, hormones, vaccines, and other pharmaceutical products
XX      of vaccines, healthcare products like human hemoglobin, industrial or
XX      household enzymes. Plants which can be transformed with the constructs

```

```

CC      of the invention include maize, millet, sorghum, sugar cane, rice,
CC      wheat, barley, oat, rye or turf grass.
XX
XX      Sequence 5263 BP; 1377 A; 1326 C; 1144 G; 1416 T; 0 other;
XX
XX      Query Match      100.0%; Score 182; DB 21; Length 5263;
XX      Best Local Similarity 100.0%; Pred. No. 4.3e-50;
XX      Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 GAGCTCGCTCCCGCCCGCTGTCATATGAGATGATAAGCGCTGCTGGGATTCAGCGTG 60
DB      3857 GAGCTCGCTCCCGCCCGCTGTCATATGAGATGATAAGCGCTGCTGGGATTCAGCGTG 3798
QY      61 AGGGGGCAGGAGTGGCTTATTTCTGGGAGGAGACACACAGCGTTCCCACTACAAATA 120
DB      3797 AGGGGGCAGGAGTGGCTTATTTCTGGGAGGAGACACACAGCGTTCCCACTACAAATA 3738
QY      121 ATTTTGTAACTTTAAGAGGAGATACATATATGCGAAGCATGACTGCTGGACAGGCTA 180
DB      3737 ATTTTGTAACTTTAAGAGGAGATACATATATGCGAAGCATGACTGCTGGACAGGCTA 3678
QY      181 GC 182
DB      3677 GC 3676

RESULT 4
AAZ61374
ID      AAZ61374 standard; DNA; 182 BP.
XX
XX      AC      AAZ61374;
XX
XX      19-JUN-2000 (first entry)
XX
XX      Nucleotide sequence of chimeric promoter pRrnlU7g10+DB/pt.
XX
XX      Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW      Rrnl promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
XX
XX      Synthetic.
XX
XX      Key
FH      Promoter
FT      7..89
FT      /tag= a
FT      /note= "Rrnl plastid promoter"
FT      misc_signal
FT      141..144
FT      /tag= b
FT      /note= "Shine-Dalgarno sequence"
XX
XX      WO200007431-A1.
XX
XX      17-FEB-2000.
XX
XX      03-AUG-1999; 99WO-US17806.
XX
XX      03-AUG-1998; 98US-0095163.
XX
XX      03-AUG-1998; 98US-0095167.
XX
XX      15-DEC-1998; 98US-0112257.
XX
XX      29-APR-1999; 98US-0131611.
XX
XX      11-JUN-1999; 98US-0138764.
XX
XX      (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX      Maliga P, Kuroda H, Khan MS;
PI
XX      WPI; 2000-205525/18.
XX
XX      New recombinant DNA constructs, for expressing high levels of
XX      heterologous protein in plastids of higher plants, includes promoter, a
XX      leader sequence and a downstream box element -
XX
XX      Claim 4; Fig 3D; 164pp; English.

```

CC The present sequence represents a chimeric plastid rRNA operon  
 CC of type Prn7g10, derived with the T7 phage gene and Escherichia coli  
 CC deoxyribose box. The chimeric construct is designed to express  
 CC heterologous proteins in the plastids of higher plants. The DNA  
 CC constructs comprise a 5' regulatory region which includes a promoter  
 CC to a coding region for the heterologous protein. The DNA  
 CC region enhances translational efficiency of an mRNA molecule encoded by  
 CC the DNA construct. The DNA constructs are used for producing protein  
 CC monocot and dicot plants having high levels of heterologous protein  
 CC on an industrial or pharmaceutical scale. Expression of proteins with  
 CC agronomic, industrial or pharmaceutical value. The DNA constructs  
 CC of vaccines, healthcare products like human haemoglobin, industrial or  
 CC household enzymes. Plants which can be transformed with the constructs  
 CC of wheat, barley, oat, rye or turf grass.

XX Sequence 182 BP; 47 A; 38 C; 52 G; 45 T; 0 other;

Query Match Similarity 90.3%; Score 164.4; DB 21; Length 182;  
 Matches 171; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCTCGCTCCCGCCGCTGTCATAGAGATGGATAGAGCTCGTGGGATTCAGCTG 60  
 Db 1 GAGCTCGCTCCCGCCGCTGTCATAGAGATGGATAGAGCTCGTGGGATTCAGCTG 60  
 QY 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGACACACAGCTTCCCTAGAAATA 120  
 Db 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGACACACAGCTTCCCTAGAAATA 120  
 QY 121 ATTTTGTTTAACTTTAAGAGAGATATACATATGCGACGATGCTGGTGGACGCTA 180  
 Db 121 ATTTTGTTTAACTTTAAGAGAGATATACATATGCGACGATGCTGGTGGACGCTA 180  
 QY 181 GC 182  
 Db 181 GC 182

# RESULT 5

AAZ61375  
 ID AAZ61375 standard; DNA: 161 BP.

XX AAZ61375;

XX 19-JUN-2000 (first entry)

XX Nucleotide sequence of chimeric promoter Prn7g10-DB.

XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;  
 KW Prn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT Promoter 7..89

FT misc\_signal /note= "Prn plastid promoter"

FT /tag= "a"

FT /tag= "b"

FT /note= "Shine-Dalgarno sequence"

XX W0200007431-AL.

XX 17-FEB-2000.

XX 03-AUG-1999; 99WO-US17806.

XX 03-AUG-1998; 98US-0095163.

XX 03-AUG-1998; 98US-0095167.

XX 15-DEC-1998; 98US-0112257.

PR 29-APR-1999; 99US-0131611.  
 XX 11-JUN-1999; 99US-0138784.  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Malliga P, Kuroda H, Khan MS;

XX WPI: 2000-205525/18.

XX New recombinant DNA constructs, for expressing high levels of  
 PT heterologous protein in plastids of higher plants, includes promoter, a  
 PT leader sequence and a downstream box element -

XX Claim 4; fig 3b; 164pp; English.

XX The present sequence represents a chimeric plastid rRNA operon  
 CC omega-type (Prn7) promoter with the T7 phage gene and a synthetic  
 CC deoxyribose box. The chimeric construct is designed to express  
 CC heterologous proteins in the plastids of higher plants. The DNA  
 CC constructs comprise a 5' regulatory region which includes a promoter  
 CC to a coding region for the heterologous protein. The DNA  
 CC region enhances translational efficiency of an mRNA molecule encoded by  
 CC the DNA construct. The DNA constructs are used for producing protein  
 CC monocot and dicot plants having high levels of heterologous protein  
 CC on an industrial or pharmaceutical scale. Expression of proteins with  
 CC agronomic, industrial or pharmaceutical value. The DNA constructs  
 CC of vaccines, healthcare products like human haemoglobin, industrial or  
 CC household enzymes. Plants which can be transformed with the constructs  
 CC of wheat, barley, oat, rye or turf grass.

XX Sequence 161 BP; 43 A; 30 C; 48 G; 40 T; 0 other;

Query Match Similarity 97.6%; Score 159.4; DB 21; Length 161;  
 Matches 160; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCTCGCTCCCGCCGCTGTCATAGAGATGGATAGAGCTCGTGGGATTCAGCTG 60  
 Db 1 GAGCTCGCTCCCGCCGCTGTCATAGAGATGGATAGAGCTCGTGGGATTCAGCTG 60  
 QY 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGACACACAGCTTCCCTAGAAATA 120  
 Db 61 AGGGGCGAGGATGCTATATTTCTGGGAGGAGACACACAGCTTCCCTAGAAATA 120  
 QY 121 ATTTTGTTTAACTTTAAGAGAGATATACATATGCGACG 161  
 Db 121 ATTTTGTTTAACTTTAAGAGAGATATACATATGCGTAGC 161

# RESULT 6

AAZ88175  
 ID AAZ88175 standard; DNA: 168 BP.

XX AAZ88175;

XX 25-APR-2000 (first entry)

XX Prn7g10L fusion nucleic acid sequence.

XX Tobacco; ribosome binding site; aptotinin; herbicide tolerance; plastid;  
 KW human growth hormone; insulin; ds.

XX Nicotiana sp.

XX Synthetic.

XX W0200003022-A2.

XX 20-JAN-2000.

XX 10-JUL-1999; 99WO-US15472.



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XX PR 10-JUL-1998; 98US-0113257.
XX XX (CALJ ) CALGENE LLC.
XX PI Hajdukiewicz P, McBride KE, Nehra N, Schaaf DJ, Stalker DM;
XX PI Staub JM, Ye G;
XX DR WPI; 2000-147617/13.
XX XX
XX PT New construct useful for producing herbicide tolerance in plants and
XX PT for directing production of pharmaceutical proteins
XX PR Example 1; Fig 6; 62pp; English.
XX CC The present invention describes a construct (I) comprising a plant
XX CC plastid promoter region, a DNA sequence capable of conferring herbicide
XX CC tolerance in the plant cell and a transcription termination region
XX CC operably joined in the 5'-3' direction. (I) is useful for producing
XX CC herbicide tolerance in a plant cell, comprising transforming plastids of
XX CC the plant cell with (I) and the herbicide tolerance is useful for
XX CC expression of non-transgenic plants. (I) comprises a DNA sequence
XX CC encoding enzymes involved in herbicide tolerance or for producing
XX CC pharmaceutical proteins e.g. human growth hormone, aprotinin, insulin or
XX CC insulin precursors. Transplastomic plants have high level of tolerance to
XX CC herbicides. Protein levels obtained from plastid expression constructs
XX CC is found to be higher than from nuclear expression constructs. Plastid
XX CC expression constructs utilising 16S ribosomal RNA operon (Prn)/G10L
XX CC promoter/RBS sequence accumulates 50-3500 fold higher levels of protein
XX CC than nuclear expression constructs, by including targeting sequences,
XX CC that direct the expression of the protein to the plastid. The plastid
XX CC regions for e.g. thylakoid membrane, which facilitates increased
XX CC oxidative stability and proper protein folding. Insect or disease
XX CC resistance gene can also be included in the herbicide tolerance
XX CC constructs. The present sequence represents a Prn/G10L fusion nucleic
XX CC acid sequence, which is used in an example from the present invention
XX CC for the production of expression constructs.
XX SQ Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
XX
Query Match 61.1%; Score 111.2; DB 21; Length 168;
Best Local Similarity 88.7%; Pred. No. 3.8e-27;
Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;
OY 7 GCTCCCGCCGCGTTCATGAGATGATAGAGGCTCGTGGGATTCACGTGAGGGG 66
DB 23 GCTCCCGCCGCGTTCATGAGATGATAGAGGCTCGTGGGATTCACGTGAGGGG 82
OY 67 CAGGATGCGGTATATTTCTGGGAGGAGACACACGCTTCCCACTAGAAATATTTTG 126
DB 83 CAGGATGCGGTATATTTCTGGGAGGAGCA----ACTCCGGCGCAATTTGTAAGAAATATTTTG 138
DB 127 TTTACTTTAAGAGGAGATATACATATGG 156
DB 139 TTTACTTTAAGAGGAGATATACCATGG 168
OY 127 TTTACTTTAAGAGGAGATATACATATGG 156
DB 139 TTTACTTTAAGAGGAGATATACCATGG 168
RESULT 7
AAF25352
ID AAF25352 standard; DNA: 168 BP.
XX AC AAF25352;
XX XX
XX DE 30-APR-2001 (first entry)
XX XX
XX DE Nucleotide sequence of Prn/G10L promoter/RBS hybrid.
XX XX Plant plastid; herbicide tolerance; RPSPS protein;
XX KW G10L ribosome binding site; ds.
XX OS Synthetic.
XX XX

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PN WO200104327-A1.
XX PR 18-JAN-2001.
XX XX
XX XX 10-JUL-2000; 2000WO-US18727.
XX XX 10-JUL-1999; 99US-0351123.
XX XX (CALJ ) CALGENE LLC.
XX XX
XX XX Hajdukiewicz P;
XX XX WPI; 2001-138356/14.
XX XX
XX PT Novel constructs for expressing herbicide tolerance genes in plant cell
XX PT plastids, comprises a promoter functional in plant plastid, a DNA
XX XX sequence conferring herbicide tolerance and transcription terminator -
XX XX Example 1; Fig 6; 70pp; English.
XX CC The specification describes a construct comprising a promoter functional
XX CC in a plant plastid, a DNA sequence capable of conferring tolerance in a
XX CC plant cell, a DNA sequence capable of conferring tolerance in a
XX CC region, in the 5'-3' direction of transcription. The construct is useful
XX CC for producing tolerance of a herbicide in a plant cell. The construct is
XX CC also useful for enhancing expression of a wide variety of genes, both
XX CC eukaryotic and prokaryotic, in plant plastids. It is useful for genetic
XX CC engineering of plant cells and which provide for enhanced expression of
XX CC EPSPS proteins or hch protein in plant cell plastids. The present
XX CC sequence represents a hybrid comprising plastid 16S ribosomal RNA
XX CC operon, and a synthetic chlo. ribosome binding site (RBS). The hybrid
XX CC is used to produce constructs of the invention.
XX SQ Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
XX
Query Match 61.1%; Score 111.2; DB 22; Length 168;
Best Local Similarity 88.7%; Pred. No. 3.8e-27;
Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;
OY 7 GCTCCCGCCGCGTTCATGAGATGATAGAGGCTCGTGGGATTCACGTGAGGGG 66
DB 23 GCTCCCGCCGCGTTCATGAGATGATAGAGGCTCGTGGGATTCACGTGAGGGG 82
OY 67 CAGGATGCGGTATATTTCTGGGAGGAGACACACGCTTCCCACTAGAAATATTTTG 126
DB 83 CAGGATGCGGTATATTTCTGGGAGGCA----ACTCCGGCGCAATTTGTAAGAAATATTTTG 138
OY 127 TTTACTTTAAGAGGAGATATACATATGG 156
DB 139 TTTACTTTAAGAGGAGATATACCATGG 168
RESULT 8
AAF57902
ID AAF57902 standard; DNA: 168 BP.
XX AC AAF57902;
XX XX
XX DE 18-APR-2001 (first entry)
XX XX
XX DE Prn/G10L promoter/RBS hybrid coding sequence.
XX XX Green fluorescent protein; GFP; translational fusion; gene expression;
XX KW herbicide tolerance; pharmaceutical protein; disease resistance; ds.
XX OS Synthetic.
XX XX
XX XX WO200104331-A2.
XX XX 18-JAN-2001.
XX PD 26-JUN-2000; 2000WO-US18096.
XX PF

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XX 09-JUL-1999; 99US-0351124.
PR (CALJ ) CALGENE L.C.
PA
XX Staub JM;
XX WPI, 2001-147195/15.
XX
XX New constructs encoding translational fusion of 14 amino acids derived
PT from green fluorescent protein for enhancing desired protein
PT (3-enoilpruvyilshikimate-3-phosphate synthase) expression in plant cells
PT
XX
XX Example 1: Fig 1: 27pp; English.
PS
XX The present invention describes a construct comprising a promoter region,
CC a DNA sequence encoding at least the first 5 amino acids of green
CC fluorescent protein (GFP), a DNA sequence encoding a protein of interest
CC and a transcription termination region. Constructs of this type have been
CC shown to enhance gene expression, and they can be used in plants
CC to produce pharmaceuticals and the ability to produce
CC pharmaceutically important proteins on the plant.
XX
XX Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
SQ
Query Match 61.1%; Score 111.2; DB 21; Length 168;
Best Local Similarity 88.7%; Pred. NO. 3.8e-27;
Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;
XX
XX 7 GTCGCGCGCGCTGCTCAATGATGATAGAGCGCTGCGGATTCAGCTGAGCGGG 66
DB * 23 GCTCCCGCGCGCTGCTCAATGATGATAGAGCGCTGCGGATTCAGCTGAGCGGG 82
XX
XX 67 CAGGGATGCTATATTTCTGGAGGAGGACACACGCTTCCGACGTAGAAATATTG 126
DB 83 CAGGATGCTATATTTCTGGAGGAGGACACACGCTTCCGACGTAGAAATATTG 138
XX
XX 127 TTTAACTTTAAGAGGAGATATACATATGG 156
DB 139 TTTAACTTTAAGAGGAGATATACATATGG 168
XX
XX
XX RESULT 9
XX AAZ61361 standard; DNA; 191 BP.
XX
XX AAZ61361;
XX
XX 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of chimeric promoter PrnLatp-DB.
XX
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW Prn promoter; atp; protein expression; vaccine; enzyme; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Promoter /tag= a
XX misc_signal 114..116 /note= "Prn plastid promoter"
XX /tag= a
XX /note= "Shine-Dalgarno sequence"
XX
XX WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1999; 98US-0095163.
XX

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03-AUG-1998; 98US-0095167.
15-DEC-1998; 98US-0112257.
29-APR-1999; 99US-0131611.
PR 11-JUN-1999; 99US-0138764.
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX WPI, 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
PT heterologous protein in plastids of higher plants, includes promoter, a
PT leader sequence and a downstream box element -
XX
XX Claim 3; Fig 3A; 164pp; English.
XX
XX The present sequence represents a chimeric plastid rRNA operon
CC omega-type (Prn) promoter with atp translation control sequences,
CC without a downstream box element, and a downstream box element for
CC heterologous proteins in the plastids of higher plants. The DNA
CC constructs comprise a 5' regulatory region which includes a promoter
CC element, a leader sequence and a downstream box element operably
CC linked to a heterologous protein coding sequence. The DNA
CC construct enhances translational efficiency of an mRNA molecule encoded by
CC the DNA construct. The DNA constructs are used for producing transformed
CC monocot and dicot plants having high levels of heterologous protein
CC expression. They can be used to drive expression of proteins with
CC heterologous protein coding sequences in monocot and dicot plants.
CC of vaccines healthcare products like human haemoglobin, industrial or
CC household enzymes. Plants which can be transformed with the constructs
CC of the invention include maize, millet, sorghum, sugar cane, rice,
CC wheat, barley, oat, rye or turf grass.
XX
XX Sequence 191 BP; 52 A; 32 C; 48 G; 59 T; 0 other;
Query Match 51.4%; Score 93.6; DB 21; Length 191;
Best Local Similarity 75.0%; Pred. NO. 3.8e-21;
Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
XX
XX 1 GAGCTGCTGCTCCCGCGCGCTGCTCAATGAGATGATAGAGCGCTGCGGATTCAGCTG 60
DB 1 GAGCTGCTGCTCCCGCGCGCTGCTCAATGAGATGATAGAGCGCTGCGGATTCAGCTG 60
XX
XX 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGCACACACGCTTCCCTACTAGAAATA 120
DB 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGCACACACGCTTCCCTACTAGAAATA 120
XX
XX 121 ATTTTGTAACTTAAAGAGGAGATATACATATGG 156
DB 121 TATTTAAATTCGATATTTTGTAAAACATTCG 156
XX
XX
XX RESULT 10
XX ID AAZ61360 standard; DNA; 227 BP.
XX
XX AAZ61360;
XX
XX 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of chimeric promoter PrnLatp-DBwt.
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW Prn promoter; atp; protein expression; vaccine; enzyme; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Promoter /tag= a
XX /note= "Prn plastid promoter"
XX

```

```

FT misc_signal 114..116
FT /*tag= b
FT /*note= "Shine-Dalgarno sequence"
PA WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 03-AUG-1998; 98US-0112257.
XX 23-AUG-1998; 98US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX: Maliga P, Kuroda H, Khan MS;
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element
XX
XX Claim 3; Fig 3A; 164pp; English.
XX
XX The present sequence represents a chimeric plastid rRNA operon
XX omega-type (Prin) promoter with atpB translation control sequences and
XX a wild type downstream box. The chimeric promoter is used, as a 5'
XX regulatory sequence, to produce recombinant DNA constructs for expressing
XX heterologous proteins in the plastids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used to drive expression of proteins with
XX agronomic, industrial or pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes, plants which can be transformed with the constructs
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX
XX Sequence 227 BP; 58 A; 42 C; 55 G; 72 T; 0 other;
XX
Query Match 51.4%; Score 93.6; DB 21; Length 227;
Best Local Similarity 75.0%; Pred. No. 3e-21;
Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 GAGCTCGCTCCCGCGCGTTCATGAGATGATAGAGCGTCGTGGGATTGACGTG 60
DB 1 GAGCTCGCTCCCGCGCGTTCATGAGATGATAGAGCGTCGTGGGATTGACGTG 60
QY 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACACGTTTCCCACTAGAAATA 120
DB 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGATTAACCGTTCAGCTGACGGGACATT 120
QY 121 ATTTGTTTAACTTGAAGGACAGATATACATATG 156
DB 121 ATTTTAAATTCGATATTTTGCAGAAACATTTG 156
RESULT 11
AAZ61362
XX ID AAZ61362 standard; DNA: 227 BP.
XX AAZ61362;
XX
XX 19-JUN-2000 (first entry)
XX

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DE Nucleotide sequence of chimeric promoter PrlnLatpB+Dbm.
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
XX Prln promoter; atpB; protein expression; vaccine; enzyme; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 7..89
XX /*tag= a
XX /*note= "Prln plastid promoter"
XX misc_signal 114..116
XX /*tag= b
XX /*note= "Shine-Dalgarno sequence"
XX
XX WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 03-AUG-1998; 98US-0112257.
XX 23-AUG-1998; 98US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX: Maliga P, Kuroda H, Khan MS;
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element
XX
XX Claim 3; Fig 3A; 164pp; English.
XX
XX The present sequence represents a chimeric plastid rRNA operon
XX omega-type (Prin) promoter with atpB translation control sequences and
XX a mutated downstream box. The chimeric promoter is used, as a 5'
XX regulatory sequence, to produce recombinant DNA constructs for expressing
XX heterologous proteins in the plastids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used to drive expression of proteins with
XX agronomic, industrial or pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes, plants which can be transformed with the constructs
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX
XX Sequence 227 BP; 64 A; 40 C; 59 G; 64 T; 0 other;
XX
Query Match 51.4%; Score 93.6; DB 21; Length 227;
Best Local Similarity 75.0%; Pred. No. 3e-21;
Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 GAGCTCGCTCCCGCGCGTTCATGAGATGATAGAGCGTCGTGGGATTGACGTG 60
DB 1 GAGCTCGCTCCCGCGCGTTCATGAGATGATAGAGCGTCGTGGGATTGACGTG 60
QY 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACACGTTTCCCACTAGAAATA 120
DB 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGATTAACCGTTCAGCTGACGGGACATT 120
QY 121 ATTTGTTTAACTTGAAGGACAGATATACATATG 156
DB 121 ATTTTAAATTCGATATTTTGCAGAAACATTTG 156

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Db 121 TATTTTAAATCGATATTTTGCMAAACATTTGC 156
RESULT 12
AAF81268
ID AAF81268 standard; DNA; 1049 BP.
XX
XX AAF81268;
XX
Dt 05-JUN-2001 (first entry)
XX
XX DNA fragment designed for CRE-induced expression of recombinant protein.
DE
XX CRE recombinase; plasmid genome manipulation;
KW
XX site-specific recombination; ds.
XX
XX Synthetic.
XX
XX WO200121768-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25930.
XX
XX 21-SEP-1999; 99US-0155007.
XX
XX 13-JUN-2000; 2000US-0211139.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Corneille S, Lutz K;
XX
XX WPI; 2001-266071/27.
XX
XX Removing target nucleic acid sequences e.g. selectable marker genes,
XX genes involved in plant cell metabolism, growth development and
XX selection from plasmid genomes, by Cre-mediated site specific
XX recombination.
XX
XX Example 3; page 48; 83pp; English.
XX
XX The present sequence was used in an example illustrating an invention
XX relating to a method for manipulating the genome of higher plants. The
XX method involves selecting plant cells expressing proteins encoded by a
XX DNA construct having a nucleic acid encoding a marker, excision sites
XX and plasmid targeting sequence. The method is useful for removing
XX marker genes from the genome of higher plants. The method is useful for
XX heterologous sequences from the plasmid genome, such as selectable
XX marker genes following successful isolation of transformed progeny,
XX and for removing endogenous genes associated with male sterility, clp
XX ribosomal proteins and ribosomal RNA operon sequences from the plasmid
XX genome.
XX
XX Sequence 1049 BP; 269 A; 235 C; 282 G; 263 T; 0 other;
XX
XX Query Match 51.4%; Score 93.6; DB 22; Length 1049;
XX Best Local Similarity 75.0%; Pred. No. 5, 5e-21;
XX Matches 117; Conservative. 0; Mismatches 39; Indels 0; Gaps 0;
Oy 1 GAGCTCGCTCCCGCGCGCTGTAATTCCTGAGAGGAGGACACACAGCTTCCCACTAGAAATA 60
Db 1 GAGCTCGCTCCCGCGCGCTGTAATTCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
Oy 61 AGGCGCCGAGGAGATGCTATATTTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db 61 AGGCGCCGAGGAGATGCTATATTTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Oy 121 ATTTTGTACTTACTTTTGAAGAGGAGGATATACATATG 156
Db 121 TATTTTAAATCGATATTTTGCMAAACATTTGC 156
RESULT 13
AAZ61382
AAZ61382 standard; DNA; 1985 BP.
XX
XX AAZ61382;
XX
XX 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of DNA construct FLARE16-S2.
XX
XX Green fluorescent protein; GFP; asda; aptB; protein expression; vaccine;
XX haemoglobin; enzyme; psba; ss.
XX
XX Synthetic.
XX Unidentified.
XX Aequorea victoria.
XX
XX Key Location/Qualifiers
XX misc_feature 7..221 /tag= a
XX /note= "atpB downstream box"
XX /tag= b
XX /note= "aada sequence"
XX /tag= c
XX 1059..1779 /tag= c
XX /note= "green fluorescent protein region"
XX 1790..1978 /tag= d
XX /note= "psba region"
XX
XX WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX
XX 03-AUG-1998; 98US-0095167.
XX
XX 15-DEC-1998; 98US-0112257.
XX
XX 15-DEC-1998; 98US-0112257.
XX
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous proteins in plasmids of higher plants, includes promoter, a
XX leader sequence and a downstream box element.
XX
XX Disclosure; Fig 30; 164pp; English.
XX
XX The present sequence represents a DNA construct of the invention.
XX The specification describes recombinant DNA constructs for expressing
XX heterologous proteins in the plasmids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plant cells. The DNA constructs are used to drive
XX expression of proteins with economic and pharmaceutical importance,
XX of vaccines, healthcare products like human hemoglobin, industrial or
XX household enzymes. Plants which can be transformed with the constructs
XX of the invention include rice, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX
XX Sequence 1985 BP; 553 A; 431 C; 482 G; 519 T; 0 other;
XX
XX Query Match 51.4%; Score 93.6; DB 21; Length 1985;
XX Best Local Similarity 75.0%; Pred. No. 7e-21;

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Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 GAGCTGCTCCCGCCGCTGTCATGAGATGATGAGAGCTGCTGGGATGACGCG 60  
 DB 1 GAGCTGCTCCCGCCGCTGTCATGAGATGATGAGAGCTGCTGGGATGACGCG 60  
 QY 61 AGGGGCGAGGATGCTGTATATTTCTGGGAGGAGACACACGCTTCCCACTAGAAATA 120  
 DB 61 AGGGGCGAGGATGCTGTATATTTCTGGGAGGATTAACCGATGACGTGCAAGCGGACAT 120  
 QY 121 ATTTTCTTTAACTTTTAAGAGAGAGATATACATATGG 156  
 DB 121 TATTTTAAATTTGATTAATTTTTCGAACAACATTTTCG 156

RESULT 14  
 AAZ61369  
 ID AAZ61369 standard; DNA; 153 BP.  
 AC AAZ61369;  
 XX  
 XX  
 XX 19-JUN-2000 (first entry)  
 DE Nucleotide sequence of chimeric promoter Prn1psbb-DB.  
 KW Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;  
 KW Prn promoter; psbb; protein expression; vaccine; enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key  
 XX Location/Qualifiers  
 XX Promoter  
 XX /tag- a  
 XX /note- "Prn plastid promoter"  
 FT misc\_signal  
 FT 138..142  
 FT /tag- b  
 FT /note- "Shine-Dalgarno sequence"  
 XX  
 XX WO200007431-A1.  
 XX  
 XX 17-FEB-2000.  
 XX  
 XX 03-AUG-1999; 99WO-US17806.  
 XX  
 XX 03-AUG-1998; 98US-0095163.  
 XX 03-AUG-1998; 98US-0095167.  
 XX 15-DEC-1998; 98US-0112257.  
 XX 29-APR-1999; 99US-0131611.  
 XX 11-JUN-1999; 99US-0138764.  
 XX  
 XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 XX Maliga P, Kuroda H, Khan MS;  
 XX WPI; 2000-205525/18.  
 XX  
 XX New recombinant DNA constructs, for expressing high levels of  
 XX heterologous protein in plastids of higher plants, includes promoter, a  
 XX leader sequence and a downstream box element -  
 XX  
 XX Claim 3; Fig 3B; 16app; English.  
 XX  
 XX The present sequence represents a chimeric plastid rRNA operon  
 XX omega-type (Prn) promoter with psbb translation control sequences,  
 XX without a downstream box. The chimeric promoter is used, as a 5'  
 XX regulatory sequence, to produce recombinant DNA constructs for expressing  
 XX heterologous proteins in the plastids of higher plants. The DNA  
 XX constructs comprise a 5' regulatory region which includes a promoter  
 XX element a leader sequence and a downstream box element operably linked  
 XX to a coding region encoding a protein. The chimeric regulatory  
 XX region enhances translational efficiency of the protein. The chimeric  
 XX the DNA construct. The DNA constructs are used for producing transformed  
 XX monocot and dicot plants having high levels of heterologous protein

CC expression. They can be used to drive expression of proteins with  
 CC agronomic, industrial or pharmaceutical importance, including production  
 CC of vaccines, healthcare products like human haemoglobin, industrial or  
 CC household enzymes. Plants which can be transformed with the constructs  
 CC of the invention include maize, millet, sorghum, sugar cane, rice,  
 CC wheat, barley, oat, rye or turf grass.

SQ Sequence 153 BP; 36 A; 27 C; 47 G; 43 T; 0 other;  
 Query Match 50.7%; Score 92.2; DB 21; Length 153;  
 Best Local Similarity 92.4%; Pred. No. 7.6e-21;  
 Matches 97; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCTGCTCCCGCCGCTGTCATGAGATGATGAGAGCTGCTGGGATGACGCG 60  
 DB 1 GAGCTGCTCCCGCCGCTGTCATGAGATGATGAGAGCTGCTGGGATGACGCG 60  
 QY 61 AGGGGCGAGGATGCTGTATATTTCTGGGAGGAGACACACGCT 105  
 DB 61 AGGGGCGAGGATGCTGTATATTTCTGGGAGCAATGCAATAAAGTT 105

RESULT 15  
 AAZ61372  
 ID AAZ61372 standard; DNA; 185 BP.  
 AC AAZ61372;  
 XX  
 XX 19-JUN-2000 (first entry)  
 DE Nucleotide sequence of chimeric promoter Prn1psba-DB(+CC).  
 KW Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;  
 KW Prn promoter; psba; protein expression; vaccine; enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key  
 XX Location/Qualifiers  
 XX Promoter  
 XX 7..89  
 XX /tag- a  
 XX /note- "Prn plastid promoter"  
 FT misc\_signal  
 FT 144  
 FT /tag- b  
 FT /note- "Shine-Dalgarno sequence"  
 XX  
 XX WO200007431-A1.  
 XX  
 XX 17-FEB-2000.  
 XX  
 XX 03-AUG-1999; 99WO-US17806.  
 XX  
 XX 03-AUG-1998; 98US-0095163.  
 XX 03-AUG-1998; 98US-0095167.  
 XX 15-DEC-1998; 98US-0112257.  
 XX 29-APR-1999; 99US-0131611.  
 XX 11-JUN-1999; 99US-0138764.  
 XX  
 XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 XX Maliga P, Kuroda H, Khan MS;  
 XX WPI; 2000-205525/18.  
 XX  
 XX New recombinant DNA constructs, for expressing high levels of  
 XX heterologous protein in plastids of higher plants, includes promoter, a  
 XX leader sequence and a downstream box element -  
 XX  
 XX Claim 3; Fig 3C; 16app; English.  
 XX  
 XX The present sequence represents a chimeric plastid rRNA operon  
 XX omega-type (Prn) promoter with psbb translation control sequences,  
 XX without a downstream box. The chimeric promoter is used, as a 5'  
 XX regulatory sequence, to produce recombinant DNA constructs for expressing  
 XX heterologous proteins in the plastids of higher plants. The DNA  
 XX constructs comprise a 5' regulatory region which includes a promoter  
 XX element a leader sequence and a downstream box element operably linked  
 XX to a coding region encoding a protein. The chimeric regulatory  
 XX region enhances translational efficiency of the protein. The chimeric  
 XX the DNA construct. The DNA constructs are used for producing transformed  
 XX monocot and dicot plants having high levels of heterologous protein

CC heterologous proteins in the plastids of higher plants. The DNA  
 CC element, a leader sequence and a downstream box element operably linked  
 CC to a coding region of the heterologous protein. The chimeric regulatory  
 CC region enhances translational efficiency of an mRNA molecule encoded by  
 CC the DNA construct. The DNA constructs are used for producing transformed  
 CC plants and for producing heterologous proteins in plants. The plants  
 CC expression they can be used to drive expression of proteins with  
 CC agronomic, industrial or pharmaceutical importance, including production  
 CC of vaccines, healthcare products like human haemoglobin, industrial or  
 CC household enzymes. Plants which can be transformed with the constructs  
 CC include cereals such as wheat, maize, sorghum, sugar cane, rice,  
 CC wheat, barley, oat, rye or turf grass.

XX  
 SQ Sequence 185 BP; 47 A; 35 C; 51 G; 52 T; 0 other;

Query Match 50.7%; Score 92.2; DP 21; Length 185;

Best Local Similarity 88.5%; Pctd No. 8.2e-21;

Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GAGCTGCTCCCGCCCGCTGCTCAATGAGATGATAGAGGCTGTGGGATTGACGTG 60

Db 1 GAGCTGCTCCCGCCCGCTGCTCAATGAGATGATAGAGGCTGTGGGATTGACGTG 60

QY 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACGGTTCCCACT 113

Db 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACGGTTCCCACT 113

QY 62 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACGGTTCCCACT 113

Db 62 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACCAACGGTTCCCACT 113

Search completed: May 25, 2003, 13:45:18

Job time : 213 secs